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(54) Title: GENETICALLY MODIFIED CELLS AND METHODS FOR EXPRESSING RECOMBINANT HEPARANASE AND METHODS OF PURIFYING SAME

(57) Abstract

Bacterial, yeast and animal cells and methods for overexpressing recombinant heparanase in cellular systems, methods of purifying recombinant heparanase therefrom and modified heparanase species which serve as precursors for generating highly active heparanase by proteolysis.

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GENETICALLY MODIFIED CELLS AND METHODS FOR EXPRESSING RECOMBINANT HEPARANASE AND METHODS OF PURIFYING SAME

FIELD AND BACKGROUND OF THE INVENTION

The present invention relates to genetically modified cells overexpressing recombinant heparanase, to methods of overexpressing recombinant heparanase in cellular systems and to methods of purifying recombinant heparanase. The invention further relates to nucleic acid constructs for directing the expression of modified heparanase species to which a protease recognition and cleavage sequence has been introduced, to the modified heparanase species expressed therefrom and to their proteolytic products. The invention further relates to *in vivo* methods of inhibiting heparanase activity.

The extracellular matrix (ECM) acts both as a structural scaffold and as an informational medium. Its dynamic status is determined by cells that secrete both its constituent molecules and enzymes that catalyze the degradation of these molecules. A stasis between ECM degrading enzymes and their inhibitors maintains the integrity of the matrix. While controlled ECM remodeling is fundamental to normal processes, uncontrolled disruption underlies diverse pathological conditions.

Among the integral constituents of basement membrane and ECM are cell adhesion molecules such as laminin and fibronectin, structural components like collagen and ellastin, and proteoglycans including sydecan, serglican, proteoglycan I and II versican (1-2).

Brief overview on recombinant gene expression:

For biochemical characterization of a protein and pharmaceutical applications, it is often necessary to overproduce and purify large quantities of the protein. A major consideration when setting up a production scheme for a recombinant protein is whether the product should be expressed intracellularly or if a secretion system can be used to direct the protein to the growth medium. The inherent properties of the protein and the intended applications dictate the expression system of choice. Another consideration when attempting the production of recombinant eukaryotic proteins are the folding and post translational modification processes associated with their natural expression.

Preferably, production is carried out in a cellular system that supports appropriate transcription, translation, and post-translation modification of the protein of interest. Thus, cultured mammalian cells are

widely used in applied biotechnology as well as in different disciplines of basic sciences of cellular and molecular biology for producing recombinant proteins of mammalian origin.

One of the most widely used cells for recombinant protein expression, particularly for biotechnological applications, is the Chinese hamster ovary cell line (CHO). Alternatively, baby hamster kidney cells (BHK21), Namalwa cells, Dauidi cells, Raji cells, Human 293 cells, Hela cells, Ehrlich's ascites cells, Sk-Hep1 cells, $MDCK_1$ cells, $MDBK_1$ cells, Vero cells, Cos cells, CV-1 cells, NIH3T3 cells, L929 cells and BLG cells (mouse melanoma) have also been shown to consecutively express large quantities of recombinant proteins.

These cells are easily transfected with foreign DNA, that can integrate into the host genome to create stable cell lines, with new acquired characteristics (i.e. expression of recombinant proteins). These new cell lines originate from a single cell that has undergone foreign DNA incorporation and are therefore referred to as "cellular clones".

Since integration of foreign DNA in host cell genome is relatively inefficient, the isolation of cellular clones requires a selection system that discriminates between the stably transformed and the primary cells.

Dihydrofolate reductase deficiency in CHO cells (CHO *dhfr*- cell line) offers a particularly convenient selection system for cellular clones. Transfection of the *dhfr* gene along with the gene of interest, results in the survival of clones in a growth medium containing methotrexate (MTX). The higher the number of foreign *dhfr* gene copies in the cellular clone, the higher the MTX concentration the cells can survive. It has been demonstrated that integration events of foreign DNA into host cell genome often maintain all the components of the transfected DNA. e.g., the selection marker as well as the gene of interest (67).

In contrast to mammalian expression systems, that inherently express limited quantities of recombinant proteins, other expression systems, such as bacteria, yeast, and virus infected insect cells are widely used.

Using such cellular gene expression systems, large amounts of either active or non-active protein can be obtained and used for biochemical analysis of protein properties, structure function relationship, kinetic studies, identification of, screening for, or production of specific inhibitors, production of poly- and monoclonal antibodies recognizing the protein, pharmaceutical applications and the like.

Bacteria are the most powerful tool for the production of recombinant proteins. A recombinant protein that is overproduced in a bacterial system might constitute up to 30 % of the total protein content of the cells. The recombinant protein accumulates in inclusion bodies where it is relatively pure (comprises up to 50 % of the protein content of the bodies) and protected from protease degradation.

Inclusion bodies enable the accumulation of up to 0.2 grams of protein per liter fermentation culture.

Using specific expression vectors, bacteria can also be directed to produce and secrete proteins into the periplasm and therefrom into the growth medium. Although the reported production quantities are not as high as in inclusion bodies, purification of the expressed protein may be simpler (68).

These advantages and the relative simple growth conditions required for bacteria to thrive, made bacteria a powerful and widely used cellular expression system for the production of recombinant proteins of interest (e.g., human α-interferon, human β-interferon, GM-CSF, G-CSF, human LNF-γ, IL-2, IL-3, IL-6, TNF, human insulin, human growth hormone, etc.).

Furthermore, non-active bacterialy produced recombinant proteins due to inappropriate folding and disulfide bonding may be reduced and/or denatured and thereafter deoxidized and/or refolded to acquire the catalytically active conformation.

However, when glycosylation of the protein is essential for its activity or uses, eukaryotic expression systems are required.

Yeasts are eukaryotic microorganisms which are widely used for commercial production of recombinant proteins. Examples include the production of insulin, human GM-CSF and hepatitis B antigens (for vaccination) by the yeast *Saccharomyces cerevisiae*. The relatively simple growth conditions and the fact that yeasts are eukaryotes make the yeast gene expression system highly suitable for the production of recombinant proteins, primarily those with pharmaceutical relevance.

In recent years methylotrophic yeasts (e.g., *Pichia pastoris*, *Hansenula polymorpha*) became widely used, thus replacing in many cases the more traditionally used yeast *Saccharomyces cerevisiae*.

Methylotrophic yeasts can grow to a high cellular density, and express and if appropriately, secrete, high levels of recombinant proteins. Quantities of the secreted, correctly-folded recombinant protein can

accumulate up to several grams per liter culture. These advantages make *Pichia pastoris* suitable for an efficient production of recombinant proteins (69).

One aspect of the present invention thus concerns the expression of recombinant heparanase in cellular systems.

heparan sulfate proteoglycans (HSPGs):

HSPGs are ubiquitous macromolecules associated with the cell surface and extracellular matrix (ECM) of a wide range of cells of vertebrate and invertebrate tissues (3-7). The basic HSPG structure consists of a protein core to which several linear heparan sulfate chains are covalently attached. The polysaccharide chains are typically composed of repeating hexuronic and D-glucosamine disaccharide units that are substituted to a varying extent with N- and O-linked sulfate moieties and N-linked acetyl groups (3-7). Studies on the involvement of ECM molecules in cell attachment, growth and differentiation revealed a central role of HSPGs in embryonic morphogenesis, angiogenesis, metastasis, neurite outgrowth and tissue repair (3-7). The heparan sulfate (HS) chains, which are unique in their ability to bind a multitude of proteins, ensure that a wide variety of effector molecules cling to the cell surface (6-8). HSPGs are also prominent components of blood vessels (5). In large vessels they are concentrated mostly in the intima and inner media, whereas in capillaries they are found mainly in the subendothelial basement membrane where they support proliferating and migrating endothelial cells and stabilize the structure of the capillary wall. The ability of HSPGs to interact with ECM macromolecules such as collagen, laminin and fibronectin, and with different attachment sites on plasma membranes suggests a key role for this proteoglycan in the self-assembly and insolubility of ECM components, as well as in cell adhesion and locomotion. Cleavage of HS may therefore result in disassembly of the subendothelial ECM and hence may play a decisive role in extravasation of normal and malignant blood-borne cells (9-11). HS catabolism is observed in inflammation, wound repair, diabetes, and cancer metastasis, suggesting that enzymes which degrade HS play important roles in pathologic processes.

Heparanase:

Heparanase is a glycosylated enzyme that is involved in the catabolism of certain glycosaminoglycans. It is an endo-β-glucuronidase that cleaves heparan sulfate at specific intrachain sites (12-15). Interaction of T and B lymphocytes, platelets, granulocytes, macrophages and mast cells with the subendothelial extracellular matrix (ECM) is associated with degradation of heparan sulfate by heparanase activity (16). Connective tissue activating peptide III (CTAP), an α-chemokine, was found to have heparanase-like activity. Placenta heparanase acts as an adhesion molecule or as a degradative enzyme depending on the pH of the microenvironvent (17).

Heparanase is released from intracellular compartments (e.g., lysosomes, specific granules) in response to various activation signals (e.g., thrombin, calcium ionophores, immune complexes, antigens and mitogens), suggesting its regulated involvement in inflammation and cellular immunity responses (16).

It was also demonstrated that heparanase can be readily released from human neutrophils by 60 minutes incubation at 4 °C in the absence of added stimuli (18).

Gelatinase, another ECM degrading enzyme which is found in tertiary granules of human neutrophils with heparanase, is secreted from the neutrophils in response to phorbol 12-myristate 13-acetate (PMA) treatment (19-20).

In contrast, various tumor cells appear to express and secrete heparanase in a constitutive manner in correlation with their metastatic potential (21).

Degradation of heparan sulfate by heparanase results in the release of heparin-binding growth factors, enzymes and plasma proteins that are sequestered by heparan sulfate in basement membranes, extracellular matrices and cell surfaces (22-23).

Purification of natural heparanase:

Heparanase activity has been described in a number of cell types including cultured skin fibroblasts, human neutrophils, activated rat T-lymphocytes, normal and neoplastic murine B-lymphocytes, human monocytes and human umbilical vein endothelial cells, SK hepatoma cells, human placenta and human platelets.

A procedure for purification of natural heparanase was reported for SK hepatoma cells and human placenta (U.S. patent No. 5,362,641) and for

human platelets derived enzymes (62). Purification was performed by a combination of ion exchange and various affinity columns including Con-A Sepharose, Blue A-agarose, Zn^{++}-chelating agarose and Heparin-Sepharose. Evidently, the amounts of active heparanase recovered by these methods is low.

Cloning and expression of the heparanase gene:

A purified fraction of heparanase isolated from human hepatoma cells was subjected to tryptic digestion. Peptides were separated by high pressure liquid chromatography (HPLC) and micro sequenced. The sequence of one of the peptides was used to screen data bases for homology to the corresponding back translated DNA sequence. This procedure led to the identification of a clone containing an insert of 1020 base pairs (bp) which included an open reading frame of 963 bp followed by 27 bp of 3' untranslated region and a poly A tail. The new gene was designated *hpa*. Cloning of the missing 5' end of *hpa* was performed by PCR amplification of DNA from placenta cDNA composite. The joined *hpa* cDNA (also referred to as p*hpa*) fragment contained an open reading frame which encodes a polypeptide of 543 amino acids with a calculated molecular weight of 61,192 daltons. Cloning an extended 5' sequence was enabled from the human SK-hep1 cell line by PCR amplification using the Marathon RACE system. The 5' extended sequence of the SK-hep1 *hpa* cDNA was assembled with the sequence of the *hpa* cDNA isolated from human placenta. The assembled sequence contained an open reading frame which encodes a polypeptide of 592 amino acids with a calculated molecular weight of 66,407 daltons. The cloning procedures are described in length in U.S. Pat. application Nos. 08/922,170, 09/109,386, and 09/258,892, the latter is a continuation-in-part of PCT/US98/17954, filed August 31, 1998, all of which are incorporated herein by reference.

The ability of the *hpa* gene product to catalyze degradation of heparan sulfate (HS) *in vitro* was examined by expressing the entire open reading frame of *hpa* in High five and Sf21 insect cells, and the mammalian human 293 embryonic kidney cell line expression systems. Extracts of infected cells were assayed for heparanase catalytic activity. For this purpose, cell lysates were incubated with sulfate labeled, ECM-derived HSPG (peak I), followed by gel filtration analysis (Sepharose 6B) of the reaction mixture. While the substrate alone consisted of high molecular weight material, incubation of the HSPG substrate with lysates of cells infected with *hpa* containing virus resulted in a complete conversion of the

high molecular weight substrate into low molecular weight labeled heparan sulfate degradation fragments (see, for example, U.S. Pat. application No. 09/071,618, which is incorporated herein by reference.

In subsequent experiments, the labeled HSPG substrate was incubated with the culture medium of infected High Five and Sf21 cells. Heparanase catalytic activity, reflected by the conversion of the high molecular weight HSPG substrate into low molecular weight HS degradation fragments, was found in the culture medium of cells infected with the pF*hpa* virus, but not the control pF1 virus.

Altogether, these results indicate that the heparanase enzyme is expressed in an active form by cells infected with Baculovirus or mammalian expression vectors containing the newly identified human *hpa* gene.

In other experiments, it was demonstrated that the heparanase enzyme expressed by cells infected with the pF*hpa* virus is capable of degrading HS complexed to other macromolecular constituents (e.g., fibronectin, laminin, collagen) present in a naturally produced intact ECM (see U.S. Pat. application No. 09/109,386, which is incorporated herein by reference), in a manner similar to that reported for highly metastatic tumor cells or activated cells of the immune system (7, 8)

Involvement of Heparanase in Tumor Cell Invasion and Metastasis:

Circulating tumor cells arrested in the capillary beds often attach at or near the intercellular junctions between adjacent endothelial cells. Such attachment of the metastatic cells is followed by rupture of the junctions, retraction of the endothelial cell borders and migration through the breach in the endothelium toward the exposed underlying base membrane (BM) (24). Once located between endothelial cells and the BM, the invading cells must degrade the subendothelial glycoproteins and proteoglycans of the BM in order to migrate out of the vascular compartment. Several cellular enzymes (e.g., collagenase IV, plasminogen activator, cathepsin B, elastase, etc.) are thought to be involved in degradation of BM (25). Among these enzymes is heparanase that cleaves HS at specific intrachain sites (16,11). Expression of a HS degrading heparanase was found to correlate with the metastatic potential of mouse lymphoma (26), fibrosarcoma and melanoma (21) cells. Moreover, elevated levels of heparanase were detected in sera from metastatic tumor bearing animals and melanoma patients (21) and in tumor biopsies of cancer patients (12).

The inhibitory effect of various non-anticoagulant species of heparin on heparanase was examined in view of their potential use in preventing extravasation of blood-borne cells. Treatment of experimental animals with heparanase inhibitors markedly reduced (> 90 %) the incidence of lung metastases induced by B16 melanoma, Lewis lung carcinoma and mammary adenocarcinoma cells (12, 13, 28). Heparin fractions with high and low affinity to anti-thrombin III exhibited a comparable high anti-metastatic activity, indicating that the heparanase inhibiting activity of heparin, rather than its anticoagulant activity, plays a role in the anti-metastatic properties of the polysaccharide (12).

Finally, heparanase externally adhered to B16-F1 melanoma cells increased the level of lung metastases in C57BL mice as compared to control mice (see U.S. Pat. application No. 09/260,037, entitled INTRODUCING A BIOLOGICAL MATERIAL INTO A PATIENT, which is a continuation in part of U.S. Pat. application No. 09/140,888, and is incorporated herein by reference.

Possible involvement of heparanase in tumor angiogenesis:

Fibroblast growth factors are a family of structurally related polypeptides characterized by high affinity to heparin (29). They are highly mitogenic for vascular endothelial cells and are among the most potent inducers of neovascularization (29-30). Basic fibroblast growth factor (bFGF) has been extracted from a subendothelial ECM produced *in vitro* (31) and from basement membranes of the cornea (32), suggesting that ECM may serve as a reservoir for bFGF. Immunohistochemical staining revealed the localization of bFGF in basement membranes of diverse tissues and blood vessels (23). Despite the ubiquitous presence of bFGF in normal tissues, endothelial cell proliferation in these tissues is usually very low, suggesting that bFGF is somehow sequestered from its site of action. Studies on the interaction of bFGF with ECM revealed that bFGF binds to HSPG in the ECM and can be released in an active form by HS degrading enzymes (33, 32, 34). It was demonstrated that heparanase activity expressed by platelets, mast cells, neutrophils, and lymphoma cells is involved in release of active bFGF from ECM and basement membranes (35), suggesting that heparanase activity may not only function in cell migration and invasion, but may also elicit an indirect neovascular response. These results suggest that the ECM HSPG provides a natural storage depot for bFGF and possibly other heparin-binding growth promoting factors (36,37). Displacement of bFGF from its storage within basement

membranes and ECM may therefore provide a novel mechanism for induction of neovascularization in normal and pathological situations.

Recent studies indicate that heparin and HS are involved in binding of bFGF to high affinity cell surface receptors and in bFGF cell signaling (38, 39). Moreover, the size of HS required for optimal effect was similar to that of HS fragments released by heparanase (40). Similar results were obtained with vascular endothelial cells growth factor (VEGF) (41), suggesting the operation of a dual receptor mechanism involving HS in cell interaction with heparin-binding growth factors. It is therefore proposed that restriction of endothelial cell growth factors in ECM prevents their systemic action on the vascular endothelium, thus maintaining a very low rate of endothelial cells turnover and vessel growth. On the other hand, release of bFGF from storage in ECM as a complex with HS fragment, may elicit localized endothelial cell proliferation and neovascularization in processes such as wound healing, inflammation and tumor development (36,37).

Recombinant heparanase for screening purposes:

Put together, the accumulated evidences indicate that a reliable and high throughput (HTS) screening system for heparanase inhibiting compounds may be applied to identify and develop non-toxic drugs for the treatment of cancer and metastasis. Research aimed at identifying and developing inhibitors of heparanase catalytic activity has been handicapped by the lack of a consistent and constant source of a purified and highly active heparanase enzyme and of a reliable screening system. Such a HTS system is described in U.S. Pat. application 09/113,168, which is incorporated herein by reference. To this end, however, methods are required for obtaining high quantities of highly pure and active heparanase, so as to enable to study the kinetics of heparanase *per se* and in the presence of potential inhibitors. The recent cloning, expression and purification of the human heparanase-encoding gene offer, for the first time, a most appropriate and reliable source of active recombinant enzyme for screening of anti-heparanase antibodies and compounds which may inhibit the enzyme and hence be applied to identify and develop drugs that may inhibit tumor metastasis, autoimmune and inflammatory diseases.

Screening for specific inhibitors using a combinatorial library:

A new approach aimed at rational drug discovery was recently developed for screening for specific biological activities. According to the

new approach, a large library of chemically diverged molecules are screened for the desired biological activity. The new approach has become an effective and hence important tool for the discovery of new drugs. The new approach is based on "combinatorial" synthesis of a diverse set of molecules in which several components predicted to be associated with the desired biological activity are systematically varied. The advantage of a combinatorial library over the alternative use of natural extracts for screening for desired biologically active compounds is that all the components comprising the library are known in advance (60).

In combinatorial screening, the number of hits discovered is proportional to the number of molecules tested. This is true even when knowledge concerning the target is unavailable. The large number of compounds, which may reach thousands of compounds tested per day, can only be screened, provided that a suitable assay involving a high throughput screening technique, in which laboratory automation and robotics may be applied, exists.

Expression of heparanase by cells of the immune system:

Heparanase catalytic activity correlates with the ability of activated cells of the immune system to leave the circulation and elicit both inflammatory and autoimmune responses. Interaction of platelets, granulocytes, T and B lymphocytes, macrophages and mast cells with the subendothelial ECM is associated with degradation of heparan sulfate (HS) by heparanase catalytic activity (10). The enzyme is released from intracellular compartments (e.g., lysosomes, specific granules) in response to various activation signals (e.g., thrombin, calcium ionophore, immune complexes, antigens, mitogens), suggesting its regulated involvement and presence in inflammatory sites and autoimmune lesions. Heparan sulfate degrading enzymes released by platelets and macrophages are likely to be present in atherosclerotic lesions (42).

Treatment of experimental animals with heparanase alternative substrates (e.g., non-anticoagulant species of low molecular weight heparin) markedly reduced the incidence of experimental autoimmune encephalomyelitis (EAE), adjuvant arthritis and graft rejection (10, 43) in experimental animals, indicating that heparanase inhibitors may be applied to inhibit autoimmune and inflammatory diseases (10,43).

The involvement of heparanase in other physiological processes and its potential therapeutic applications:

Apart from its involvement in tumor cell metastasis, inflammation and autoimmunity, mammalian heparanase may be applied to modulate bioavailability of heparin-binding growth factors (45); cellular responses to heparin-binding growth factors (e.g., bFGF, VEGF) and cytokines (IL-8) (44, 41); cell interaction with plasma lipoproteins (49); cellular susceptibility to certain viral and some bacterial and protozoa infections (45-47); and disintegration of amyloid plaques (48).

Viral Infection: The presence of heparan sulfate on cell surfaces have been shown to be the principal requirement for the binding of Herpes Simplex (45) and Dengue (46) viruses to cells and for subsequent infection of the cells. Removal of the cell surface heparan sulfate by heparanase may therefore abolish virus infection. In fact, treatment of cells with bacterial heparitinase (degrading heparan sulfate) or heparinase (degrading heparan) reduced the binding of two related animal herpes viruses to cells and rendered the cells at least partially resistant to virus infection (45). There are some indications that the cell surface heparan sulfate is also involved in HIV infection (47).

Neurodegenerative diseases: Heparan sulfate proteoglycans were identified in the prion protein amyloid plaques of Genstmann-Straussler Syndrome, Creutzfeldt-Jakob disease and Scrape (48). Heparanase may disintegrate these amyloid plaques which are also thought to play a role in the pathogenesis of Alzheimer's disease.

Restenosis and Atherosclerosis: Proliferation of arterial smooth muscle cells (SMCs) in response to endothelial injury and accumulation of cholesterol rich lipoproteins are basic events in the pathogenesis of atherosclerosis and restenosis (50). Apart from its involvement in SMC proliferation as a low affinity receptor for heparin-binding growth factors, HS is also involved in lipoprotein binding, retention and uptake (51). It was demonstrated that HSPG and lipoprotein lipase participate in a novel catabolic pathway that may allow substantial cellular and interstitial accumulation of cholesterol rich lipoproteins (49). The latter pathway is expected to be highly atherogenic by promoting accumulation of apoB and apoE rich lipoproteins (e.g., LDL, VLDL, chylomicrons), independent of feed back inhibition by the cellular cholesterol content. Removal of SMC HS by heparanase is therefore expected to inhibit both SMC proliferation

and lipid accumulation and thus may halt the progression of restenosis and atherosclerosis.

In summary, Heparanase may thus prove useful for conditions such as wound healing, angiogenesis, restenosis, atherosclerosis, inflammation, neurodegenerative diseases and viral infections. Mammalian heparanase can be used to neutralize plasma heparin, as a potential replacement of protamine. Anti-heparanase antibodies may be applied for immunodetection and diagnosis of micrometastases, autoimmune lesions and renal failure in biopsy specimens, plasma samples, and body fluids. Common use in basic research is expected.

ECM proteases and their involvement in tumor progression and metastasis:

The cooperation with pericellular proteolysis cascades is required for vascular remodeling during angiogenesis, inflammatory processes, tumor progression and metastasis. In particular, the invasive processes that occur during tumor progression - local invasion, intravasation, extravasation and metastasis formation - involve extracellular matrix (ECM) degradation by proteases.

Four classes of proteases, are known to correlate with malignant phenotype: (i) cysteine proteases including cathepsin B and L; (ii) aspartyl protease cathepsin D; (iii) serine proteases including plasmin, tissue-type plasminogen activator (tPA) and urokinase-type plasminogen activator (uPA), (iv) Matrix metalloproteinases (MMPs) including collagenases, gelatinases A and B (MMP2 and MMP9) and stromelysin (MMP3).

Cathepsins are a family of proteases that are found inside cells in normal physiological conditions. Secretion of cathepsins correlates with various pathological conditions, such as arthritis, Alzheimer's disease and cancer progression (52).

The lysosomal cystein proteases cthepsin B and L have been suggested to play a role in tumor cell invasion and spread, either by directly cleaving extracellular matrix proteins or indirectly by activating other proteases (53).

Cathepsin B was found to have elevated expression levels in cancer cells. Furthermore, the intracellular distribution of the protein differed between invasive and non-invasive cancer cells. In invasive cells, cathepsin B was found in the plasma membrane, whereas in non-invasive cells it was confined to the lysosomes (56). In human tumor cells cathepsin B was secreted from the cells (53) and was shown to degrade extracellular matrix

components (54). Cathepsin B and L have been shown to degrade type IV collagen, laminin and fibronectin *in vitro* at both acid and neutral pH (54). Both enzymes are able to activate the proenzyme form of the urokinase-type plasminogen activator (pro-uPA), which is secreted by tumor cells and can bind to receptors on the tumor cell surface (55). In this cascade mechanism, the lysosomal cysteine proteases may function as effective mediators of tumor associated proteolysis.

MMPs are a family of zinc dependent endopeptidases. They are secreted as inactive proenzymes and are activated by limited proteolysis (57). During human pregnancy, cytotrophoblasts adopt tumor-like properties: they attach the conceptus to the endometrium by invading the uterus and they initiate blood flow to the placenta by breaching maternal vessels. Matrix metalloproteinase MMP-9 (a type IV collagenase/gelatinase) was shown to be upregulated during cytotrophoblast differentiation along the invasive pathway. Furthermore, it was shown that the activity of that protease specified the ability of the cells to degrade ECM components *in vitro* (58).

Large body of evidence suggests that the matrix metalloproteinases MMP-2 and MMP-9 play an important role in tumor invasion process (59, 58).

There is clearly a widely recognized need for, and it would be highly advantageous to have, genetically modified cells overexpressing recombinant heparanase or modified species thereof, methods of overexpressing recombinant heparanase in cellular systems and methods of purifying recombinant heparanase, so as to enable, a search for heparanase inhibitors using a high throughput assay and a combinatorial approach.

SUMMARY OF THE INVENTION

According to one aspect of the present invention there is provided a recombinant cell comprising a polynucleotide sequence encoding a polypeptide having heparanase catalytic activity, the cell expressing recombinant heparanase.

According to a further aspect of the present invention, there is provided a method of obtaining recombinant heparanase comprising the steps of genetically modifying a cell with an expression vector including a polynucleotide sequence encoding a polypeptide having heparanase catalytic activity, the cell expressing recombinant heparanase.

According to still further features in the described preferred embodiments the polynucleotide sequence is as set forth in SEQ ID NO:1 or a functional part thereof, the part encodes the polypeptide having the heparanase catalytic activity.

According to still further features in the described preferred embodiments the polypeptide includes an amino acid sequence as set forth in SEQ ID NO:2 or a functional part thereof having the heparanase catalytic activity. The functional part may be the result of either genetic engineering natural processing by the transduced cell.

According to still further features in the described preferred embodiments the polynucleotide sequence is selected from the group consisting of double stranded DNA, single stranded DNA and RNA.

According to still further features in the described preferred embodiments the cell is a bacterial cell.

According to still further features in the described preferred embodiments the cell is E. *coli*.

According to still further features in the described preferred embodiments the cell is an animal cell.

According to still further features in the described preferred embodiments the animal cell is an insect cell.

According to still further features in the described preferred embodiments the insect cell is selected from the group consisting of High five and Sf21 cells.

According to still further features in the described preferred embodiments the animal cell is a mammalian cell, selected, for example, from the group consisting of a Chinese hamster ovary cell line (CHO), baby hamster kidney cells (BHK21), Namalwa cells, Dauidi cells, Raji cells, Human 293 cells, Hela cells, Ehrlich's ascites cells, Sk-Hep1 cells, $MDCK_1$ cells, $MDBK_1$ cells, Vero cells, Cos cells, CV-1 cells, NIH3T3 cells, L929 cells and BLG cells (mouse melanoma).

According to still further features in the described preferred embodiments the cell is a yeast cell.

According to still further features in the described preferred embodiments the yeast cell is a methylotrophic yeast.

According to still further features in the described preferred embodiments the yeast cell is selected from the group consisting of *Pichia pastoris*, *Hansenula polymorpha* and *Saccharomyces cerevisiae*.

According to still further features in the described preferred embodiments the heparanase is human recombinant heparanase.

According to still further features in the described preferred embodiments the polynucleotide sequence is integrated in the cell's genome rendering the cell a stably transduced.

According to still further features in the described preferred embodiments the polynucleotide sequence is external to the cell's genome, rendering the cell transiently transduced.

According to still further features in the described preferred embodiments the polynucleotide sequence forms a part of a viral genome infective to the cell, be it bacterial or animal cell.

According to still further features in the described preferred embodiments the polynucleotide sequence encodes, in addition, a signal peptide for protein secretion.

According to still further features in the described preferred embodiments the method further comprising the step of subjecting the cell to a substance which induces secretion into the growth medium of secretable proteins, thereby inducing secretion of the recombinant heparanase into the growth medium.

According to still further features in the described preferred embodiments the substance is selected from the group consisting of thrombin, calcium ionophores, immune complexes, antigens and mitogens.

According to still further features in the described preferred embodiments the calcium ionophore is calcimycin (A23187)

According to still further features in the described preferred embodiments the substance is phorbol 12-myristate 13-acetate (PMA).

According to still further features in the described preferred embodiments the method further comprising the step of purifying the recombinant heparanase.

According to still further features in the described preferred embodiments the purification is effected in part by an ion exchange (e.g., Source-S) column.

According to still further features in the described preferred embodiments the purification is from the cell.

According to still further features in the described preferred embodiments the purification is from a growth medium in which the cell is grown.

According to still further features in the described preferred embodiments the cell is grown in a large biotechnological scale of at least half a liter growth medium.

According to another aspect of the present invention provided is a method of purifying a recombinant heparanase from overexpressing cells or growth medium comprising the steps of adsorbing the recombinant heparanase on an ion exchange (e.g., Source-S) column under low salt conditions, washing the column with low salt solution thereby eluting other proteins, and eluting the recombinant heparanase from the column by a salt gradient or a higher salt concentration.

According to a further aspect of the present invention there is provided a method of activating a heparanase enzyme comprising the step of digesting the heparanase enzyme by a protease.

According to still further features in the described preferred embodiments the protease is selected from the group consisting of a cysteine protease, an aspartyl protease, a serine protease and a meatlloproteinase.

According to still further features in the described preferred embodiments the step of digesting the heparanase enzyme by a protease is effected at a pH in which the protease is active, preferably most active.

According to a further aspect of the present invention there is provided a method of *in vivo* inhibition of proteolytic processing of heparanase comprising the step of *in vivo* administering a protease inhibitor.

According to still further features in the described preferred embodiments the protease inhibitor is selected from the group consisting of a cysteine protease inhibitor, an aspartyl protease inhibitor, a serine protease inhibitor and a meatlloproteinase inhibitor.

According to a further aspect of the present invention there is provided a nucleic acid construct comprising a first nucleic acid segment encoding for an upstream portion of heparanase, a second, in frame, nucleic acid sequence encoding a recognition and cleavage sequence of a protease and a third, in frame, nucleic acid sequence encoding for a downstream portion of heparanase, wherein the second nucleic acid sequence is in between the first nucleic acid sequence and the third nucleic acid sequence.

According to still further features in the described preferred embodiments the protease is selected having no recognition and cleavage sequences in the upstream and the downstream portions of heparanase.

According to still further features in the described preferred embodiments the third nucleic acid sequence encodes for a catalytically active heparanase when correctly folded.

According to a further aspect of the present invention there is provided a precursor heparanase protein comprising an upstream portion of heparanase, a mid portion of a recognition and cleavage sequence of a protease and a downstream portion of heparanase, wherein the protease is selected having no recognition and cleavage sequences in the upstream and the downstream portions of heparanase.

According to a further aspect of the present invention there is provided a heparanase protein resulting by digesting the precursor heparanase protein described herein.

According to a further aspect of the present invention there is provided a method of obtaining a homogeneously processed, active heparanase, the method comprising the steps of (a) expressing the precursor heparanase protein in a cell which secretes the precursor heparanase protein into the growth medium to obtain a conditioned growth medium, the precursor heparanase protein including an upstream portion of heparanase, a mid portion of a recognition and cleavage sequence of a protease and a downstream portion of heparanase, wherein the protease is selected having no recognition and cleavage sequences in the upstream and the downstream portions of heparanase; (b) treating the precursor heparanase protein with the protease; and (c) purifying a proteolytic heparanase product having heparanase catalytic activity.

According to a further aspect of the present invention there is provided an antibody comprising an immunoglobulin elicited against recombinant native heparanase.

According to a further aspect of the present invention there is provided an affinity substrate comprising a solid matrix and an immunoglobulin elicited against recombinant native heparanase being immobilized thereto.

According to a further aspect of the present invention there is provided a method of affinity purifying heparanase comprising the steps of (a) loading a heparanase preparation on an affinity substrate including a solid matrix and an immunoglobulin elicited against recombinant native heparanase being immobilized thereto; (b) washing the affinity substrate; and (c) eluting heparanase molecules being adsorbed on the affinity substrate via the immunoglobulin.

The present invention successfully addresses the shortcomings of the presently known configurations by providing cells and methods for expressing recombinant heparanase, methods for purifying the recombinant heparanase and modified heparanase precursor species which can be processed to yield highly active heparanase. Other features and advantages of the various embodiments of the present invention are further addressed hereinunder.

BRIEF DESCRIPTION OF THE DRAWINGS

The invention herein described, by way of example only, with reference to the accompanying drawings, wherein:

FIG. 1 demonstrates the expression of recombinant heparanase in E. *coli* BL21(DE3)pLysS cells. Insoluble fractions of induced E. *coli* cells containing expression constructs for heparanase were analyzed on 10 % SDS-PAGE. Following electrophoresis the gel was stained with commassie blue. Lane 1 - cells transformed with pRSET (negative control), lanes 2 and 3 - cells transformed with pRSET*hpa*S1 (two different colonies). Molecular size in kDa is shown to the left (Prestained SDS-PAGE standards, Bio-Rad, CA).

FIG. 2 is a schematic presentation of the expression vector pPIC3.5K-Sheparanase. Relative positions of some restriction enzymes and genes are indicated. For the construction and utilities of pPIC3.5K-Sheparanase, see Example 2 in the Examples section below.

FIG. 3 is a schematic presentation of the expression vector pPIC9K-PP2. Positions of some restriction enzymes and genes are indicated. For the construction and utilities of pPIC3.5K-Sheparanase, see Example 2 in the Examples section below.

FIG. 4 demonstrates the secretion of human heparanase by transformed *Pichia pastoris* yeast cells. Western blot analysis using a rabbit anti-heparanase polyclonal antibody (disclosed in U.S. Pat. application No. 09/071,618, which is incorporated by reference as if fully set forth herein) was performed on culture supernatants of different transformants (with and without selection for G-418 resistance). Lane 1 - pPIC3.5K-Sheparanase transformant, lane 2 - pPIC3.5K transformant (negative control), lanes 3-6, transformants selected on 4 mg/ml of G-418. Molecular size is shown on the right as was determined using prestained SDS-PAGE standards, Bio-Rad, CA.

FIGs. 5a-e are schematic presentations of heparanase expression vectors adapted to direct heparanase expression in animal cells. *hpa* containing plasmids pS*hpa*, pS*hpa*C*dhfr*, pS1*hpa*, pS2*hpa* and pC*hpa* are of 5374 bp, 7090 bp, 6868 bp, 6892 bp and 6540 bp, respectively. SV40 prom - SV40 early promoter, CMV prom - Citomegalovirus promoter, *dhfr* - mouse dihydrofolate reductase gene, PPT - preprotrypsin signal peptide, *hpa* - heparanase cDNA sequence, *hpa*' and *hpa*'' - truncated *hpa* sequences.

FIGs. 6a-b show Western blot analysis of *hpa* transfected cells. Cell extracts (40 μg of CHO cells or 8 μg of 293 cells) were separated on 4-20 % gradient SDS-PAGE and transferred to PVDF membranes. Detection of *hpa* gene products was performed with a rabbit anti-heparanase polyclonal antibody (disclosed in U.S. Pat. application No. 09/071,739) followed by ECL detection (Amersham, UK). Figure 6a - CHO stable cellular clones (lanes 1-3) and transiently transfected 293 human cells (lane 4). Figure 6b - Mock transfected CHO cells (lane 3), CHO cells performing stable or transient expression (lanes 1 and 2, respectively). Molecular size in kDa is shown to the right, as was determined using prestained SDS-PAGE standards, Bio-Rad, CA..

FIGs. 7a-b demonstrate recombinant heparanase secretion induced by calcium ionophore and PMA. Cells of a stable CHO clone (2TT1) were induced with either calcium ionophore (Figure 7a) or PMA (Figure 7b). Condition media were collected and 20 ml loaded on SDS polyacrylamide gel followed by Western blot analysis with a rabbit anti-heparanase polyclonal antibody (disclosed in U.S. Pat. application No. 09/071,739) followed by ECL detection (Amersham, UK). Molecular size in kDa is shown on the right, as was determined using prestained SDS-PAGE standards, Bio-Rad, CA..

FIG. 7c demonstrates recombinant heparanase secretion by human 293 cells. Conditioned media of human 293 cells transfected with pS1*hpa* (lanes 3 and 4), pS2*hpa* (lanes 5 and 6) or control, untransfected cells (lanes 1 and 2), were loaded on a denaturative 4-20 % polyacrylamide gel (lanes 1, 3 and 5), or 5 fold concentrated by 10 kDa ultrafiltration tube (Intersep U.K.) (lanes 4 and 6). Heparanase was detected by Western blot analysis with a rabbit anti-heparanase polyclonal antibody (disclosed in U.S. Pat. application No. 09/071,618) followed by ECL detection (Amersham, UK). Molecular size in kDa is shown on the left, as was determined using prestained SDS-PAGE standards, Bio-Rad, CA..

FIG. 8a demonstrates heparanase activity as expressed by the ability to degrade heparin. Following overnight incubation with 50 ml unconcentrated (lanes 3, 6), 20 x concentrated (lanes 4 and 7) or 40 x concentrated (lanes 5 and 8) conditioned media, from untreated (lanes 3-5) versus treated (lanes 6-8, 2 hours of incubation with 1 mg/ml calcium ionophore) stable clones, samples were electrophoretically separated on 7.5 % polyacrylamide gel. Undegraded and degraded (by purified natural human heparanase) controls are shown in lanes 1 and 2 respectively.

FIG. 8b-c demonstrate recombinant heparanase activity following secretion induced by calcium ionophore as determined by the soluble ^{35}S-ECM degradation assay. 8b - the heparanase activity in one ml untreated conditioned media (c60), compared to one ml conditioned media treated with 100 ng/ml calcium ionophore for 24 hours (p70) from stable CHO clones was determined by the soluble ^{35}S-ECM degradation assay. 8c - the heparanase activity in one ml untreated conditioned media (c45), compared to one ml conditioned media treated with 1 mg/ml calcium ionophore for two hours (p52) from stable CHO clones was determined by the soluble ^{35}S-ECM degradation assay. Degraded substrates shift to the right.

FIGs. 8c-g show the relative heparanase activity of p70 and p52 (see Figures 8b-c) by comparing the ability of diluted (x2, x4 or x8) conditioned media to degrade ^{35}S-ECM.

FIG. 9 demonstrates glucose consumption record of heparanase producing cells in a large scale, 0.5 liters, Spinner-Basket bioreactor.

FIG. 10 demonstrates degradation of soluble sulfate labeled HSPG substrate by lysates of High five cells infected with pF*hpa*2 virus. Lysates of High five cells that were infected with pF*hpa*2 virus (•) or control pF2 virus (□) were incubated (18 h, 37 °C) with sulfate labeled ECM-derived soluble HSPG (peak I). The incubation medium was then subjected to gel filtration on Sepharose 6B. Low molecular weight HS degradation fragments (peak II) were produced only during incubation with the pF*hpa*2 infected cells, but there was no degradation of the HSPG substrate (✧) by lysates of pF2 infected cells.

FIGs. 11a-b demonstrate degradation of soluble sulfate labeled HSPG substrate by the growth medium of pF*hpa*2 and pF*hpa*4 infected cells. Culture media of High five cells infected with pF*hpa*2 (11a) or pF*hpa*4 (11b) viruses (•), or with control viruses (□) were incubated (18 h, 37 °C) with sulfate labeled ECM-derived soluble HSPG (peak I, ✧). The incubation media were then subjected to gel filtration on Sepharose 6B.

Low molecular weight HS degradation fragments (peak II) were produced only during incubation with the *hpa* gene containing viruses. There was no degradation of the HSPG substrate by the growth medium of cells infected with control viruses.

FIG. 12 presents size fractionation of heparanase activity expressed by pF*hpa*2 infected cells. Growth medium of pF*hpa*2 infected High five cells was applied onto a 50 kDa cut-off membrane. Heparanase activity (conversion of the peak I substrate, (⋄) into peak II HS degradation fragments) was found in the high (> 50 kDa) (•), but not low (< 50 kDa) (o) molecular weight compartment.

FIGs. 13a-b demonstrate the effect of heparin on heparanase activity expressed by pF*hpa*2 and pF*hpa*4 infected High five cells. Culture media of pF*hpa*2 (13a) and pF*hpa4* (13b) infected High five cells were incubated (18 h, 37 °C) with sulfate labeled ECM-derived soluble HSPG (peak I, ⋄) in the absence (•) or presence (▵) of 10 μg/ml heparin. Production of low molecular weight HS degradation fragments was completely abolished in the presence of heparin, a potent competitor for heparanase activity.

FIGs. 14a-b demonstrate degradation of sulfate labeled intact ECM by virus infected High five and Sf21 cells. High five (14a) and Sf21 (14b) cells were plated on sulfate labeled ECM and infected (48 h, 28 °C) with pF*hpa*4 (•) or control pF1 (□) viruses. Control non-infected Sf21 cells (R) were plated on the labeled ECM as well. The pH of the cultured medium was adjusted to 6.0 - 6.2 followed by 24 h incubation at 37 °C. Sulfate labeled material released into the incubation medium was analyzed by gel filtration on Sepharose 6B. HS degradation fragments were produced only by cells infected with the *hpa* containing virus.

FIGs. 15a-b demonstrate degradation of sulfate labeled intact ECM by virus infected cells. High five (15a) and Sf21 (15b) cells were plated on sulfate labeled ECM and infected (48 h, 28 °C) with pF*hpa*4 (•) or control pF1 (□) viruses. Control non-infected Sf21 cells (R) were plated on labeled ECM as well. The pH of the cultured medium was adjusted to 6.0 - 6.2, followed by 48 h incubation at 28 °C. Sulfate labeled degradation fragments released into the incubation medium was analyzed by gel filtration on Sepharose 6B. HS degradation fragments were produced only by cells infected with the *hpa* containing virus.

FIGs. 16a-b demonstrate degradation of sulfate labeled intact ECM by the growth medium of pF*hpa4* infected cells. Culture media of High five (16a) and Sf21 (16b) cells that were infected with pF*hpa*4 (•) or control

pF1 (□) viruses were incubated (48 h, 37 °C, pH 6.0) with intact sulfate labeled ECM. The ECM was also incubated with the growth medium of control non-infected Sf21 cells (R). Sulfate labeled material released into the reaction mixture was subjected to gel filtration analysis. Heparanase activity was detected only in the growth medium of pF*hpa*4 infected cells.

FIGs. 17a-b demonstrate the effect of heparin on heparanase activity in the growth medium of pF*hpa*4 infected cells. Sulfate labeled ECM was incubated (24 h, 37 °C, pH 6.0) with growth medium of pF*hpa*4 infected High five (17a) and Sf21 (17b) cells in the absence (•) or presence (V) of 10 μg/ml heparin. Sulfate labeled material released into the incubation medium was subjected to gel filtration on Sepharose 6B. Heparanase activity (production of peak II HS degradation fragments) was completely inhibited in the presence of heparin.

FIG. 18 demonstrate the purification of recombinant heparanase by a Source-S column. Lanes 1-14, 40 ml of fractions 1-14 eluted from a Source-S column. Samples were analyzed on 8-16 % gradient SDS-PAGE. Gel was stained with commassie blue.

FIG. 19 demonstrate Western blot analysis of fractions 1-14 of Figure 18. Fractions 1-14 eluted from a Source-S column were analyzed following blotting onto nitrocellulose membrane with a rabbit anti-heparanase polyclonal antibody (disclosed in U.S. Pat. application No. 09/071,739) followed by ECL detection (Amersham, UK).

FIG. 20 is a schematic presentation of plasmid pC*dhfr* that contains the mouse *dhfr* gene under CMV promoter regulation. This vector does not express heparanase and serves as negative control.

FIG. 21a demonstrates the production of heparanase in pS1*hpa* transfected BHK21 cells. Cell extracts (2 x10^5 BHK21 cells) were separated on 8-16 % gradient SDS-PAGE and transferred to PVDF membranes. Detection of *hpa* gene products was performed with a mouse anti-heparanase monoclonal antibody No. HP-117 (disclosed in U.S. Pat. application No. 09/071,739) followed by ECL detection (Amersham, UK). Molecular size in kDa is shown to the right, as was determined using prestained SDS-PAGE standards, Bio-Rad, CA. Lane 1 pS1*hpa* transfected BHK21 cells. Lane 2 control, pC*dhfr* transfected, BHK21 cells.

FIG. 21b demonstrates heparanase activity in human 293 cell extract. Cells were collected and concentrated by centrifugation (2750 x g for 5 min). The pellets were passed through three cycles of 5 minutes freezing in liquid nitrogen and thawing at 37 °C. Cell lysate was centrifuged for 15

minutes at 3000 x g, and the supernatant was collected for analysis. Increasing amounts of supernatant, between 0 and 5 μg protein per assay were assayed using the DMB activity assay described herein (see also U.S. Pat. application No. 09/113,168).

FIG. 22a demonstrates recombinant heparanase constitutive secretion by CHO cells transfected with pS1*hpa* (clone S1PPT-8). Conditioned media (20 μl) of untreated cells (lane 2), mock treated cells (lane 3) and calcium ionophore treated cells (0.1 μg/ml for 24 hours; lane 4) were electrophoresed next to a cellular extract of $1x10^5$ cells from clone 2TT1 (CHO cells transfected with pS*hpa*C*dhfr*, lane 1). Samples were separated on a 4-20 % gradient SDS-PAGE, followed by Western blot analysis with a rabbit anti-heparanase polyclonal antibody (disclosed in U.S. Pat. application No. 09/071,739) and by ECL detection (Amersham, UK). Molecular size in kDa is shown on the right, as was determined using prestained SDS-PAGE standards, Bio-Rad, CA.

FIG. 22b demonstrates recombinant heparanase constitutive secretion by CHO cells transfected with pS*hpa*C*dhfr* (2TT1 clones). Conditioned media (150 μl, concentrated by 10 kDa ultrafiltration tube) of 2TT1-2 clone (lane 2) and of clone 2TT1-8 (lane 3) were electrophoresed next to a cellular extract of $1x10^5$ cells from clone 2TT1 (lane 1). Samples were separated on a 4-20 % gradient SDS-PAGE, followed by Western blot analysis with a rabbit anti-heparanase polyclonal antibody (disclosed in U.S. Pat. application No. 09/071,739) and by ECL detection (Amersham, UK). Molecular size in kDa is shown on the right, as was determined using prestained SDS-PAGE standards, Bio-Rad, CA.

FIG. 23a demonstrates purification of recombinant heparanase from a mammalian cellular extract by ion exchange chromatography. 2TT1-8 CHO cells ($1x\ 10^8$) were extracted in 2.5 ml of 10 mM phosphate citrate buffer pH 5.4. The extract was centrifuged at 2750 x g for 5 minutes and the supernatant was collected for heparanase enzyme purification using a cation exchange chromatography column. The chromatography column (mono-S HR 5/5, Pharmacia Biotech) was equilibrated with 20 mM sodium phosphate buffer, pH 6.8, and the mixture was loaded atop thereof. Proteins were eluted from the column using a linear gradient of 0 to 1 M sodium chloride in 20 mM sodium phosphate buffer, pH 6.8. The gradient was carried out in 20 column volumes at a flow rate of one ml per minute. The elution of proteins was monitored at 214 nm and fractions of 1 ml each were

collected, starting with the first fraction (1) which was eluted after 13 minutes and which is identified by the arrowhead mark.

FIG. 23b demonstrates the presence of immunologically active recombinant heparanase in the mammalian cellular extract. An aliquot from each fraction that was collected was analyzed for the presence of the heparanase enzyme by Western blot analysis. 20 µl from each fraction, numbered 1-26, were separated on a 4-20 % SDS-PAGE. The proteins were transferred from the gel to a PVDF membrane and were detected with a monoclonal antibody No. HP-117 (disclosed in U.S. Pat. application No. 09/071,739) followed by ECL detection (Amersham, UK). Molecular size in kDa is shown to the right, as was determined using SDS-PAGE standards (M). St - a purified recombinant heparanase enzyme from CHO cells.

FIG. 23c demonstrates the presence of catalytically active recombinant heparanase in mammalian cellular extract fractions. An aliquot (30 µl) from each fraction that was collected was analyzed for heparanase activity by the DMB assay. Load - extract prior to purification. 5-7 and 16-26 correspond to fraction Nos.

FIG. 23d demonstrates a heparanase dose response. Increasing amounts from fraction No. 20, which exhibited the highest activity using the DMB assay (Figure 23c), were analyzed for heparanase activity using the tetrazolium assay, as disclosed in U.S. Pat. application No. 09/113,168.

FIG. 24a demonstrates the purification of heparanase from a mammalian cellular extract by an affinity column. A cellular extract from CHO 2TT1-8 cells was loaded on an affinity column containing antibodies elicited against native (non-denatured) recombinant heparanase. Western blot analysis of different fractions (1-6) using a monoclonal antibody No. HP-117 (disclosed in U.S. Pat. application No. 09/071,739) followed by ECL detection (Amersham, UK) is shown. Molecular size in kDa is shown to the left, as was determined using SDS-PAGE standards (M). A - recombinant heparanase enzyme purified from CHO 2TT1-8 cells on mono-S column; B - extract of 2TT1-8 cells; C - unbound, flow through proteins; and D - wash fraction proteins.

FIG. 24b demonstrates the purification of heparanase from a mammalian cellular extract by an affinity column. A cellular extract from CHO 2TT1-8 cells was loaded on an affinity column containing antibodies elicited against native (non-denatured) recombinant heparanase. Heparanase activity in affinity column fraction Nos. 1-9 was determined

using the DMB assay. Load - extract prior to purification; C - unbound, flow through proteins; and D - wash fraction proteins.

FIGs. 25a-b demonstrates proteolytic processing of heparanase from insect cells conditioned medium by protease impurities. Figure 25a shows a Western blot analysis of heparanase, following processing of the enzyme expressed in insect cells. Heparanase expressed in insect cells, partially purified on a Source-S column, was incubated for one week at 4 °C in either, 20 mM phosphate citrate buffer pH 7, containing 5 % PEG 300 (lane A), 20 mM phosphate citrate buffer pH 4, containing 5% PEG 300 and 1 x protease inhibitors cocktail (Boehringer Mannheim, Cat. No. 1836170, lane B), or 20 mM phosphate citrate buffer pH 4, containing 5% PEG 300 (lane C). M- Molecular weight markers (NEB Cat. No. 7708S). Figure 25b shows the results of DMB heparanase activity assays for the proteins.

FIGs. 25c-d demonstrate the effect of a panel of protease inhibitors on proteolytic processing and activation of heparanase expressed in insect cells. Heparanase expressed in insect cells, partially purified on a Source-S column, was incubated for one week at 4 °C in 20 mM phosphate citrate buffer, pH 4, containing 5 % PEG 300 and one of the different protease inhibitors: A - antipain; B - bestatin; C - chymostatin; D- E-64; E - leupeptin; F - pepstatin; G - phosphoramidon; H - EDTA; I - aprotinin. The treated samples were either subjected to western blot analysis (Figure 25c) or to heparanase DMB activity assay (Figure 25d). J - positive control, incubated in the absence of a protease inhibitor at pH 4; K - negative control, heparanase incubated with the same buffer at pH 7. M - Molecular weight marker (NEB Cat. No. 7708S).

FIG. 26a demonstrates proteolytic processing of heparanase secreted from insect cells by trypsin. 10 μg of heparanase, expressed in insect cells, and partially purified on a Source-S column, was incubated with increasing concentrations of trypsin (0, 1.5, 5, 10, 15 units/test, Cat. No. T-8642, Sigma USA) for 10 minutes at 25 °C. Following incubation, reaction tubes were placed on ice and 1.7 μg/ml aprotinin (trypsin inhibitor) was added. Activity was determined using the DMB assay.

FIG. 26b demonstrates a Western blot analysis of heparanase following trypsin treatment. 10 μg of heparanase, expressed in insect cells, and partially purified on a Source-S column, was incubated without (lane 1) or with 150 or 500 units of trypsin (lanes 2 and 3, respectively). A processed heparanase sample treated as described in Figure 25a-b, lanes J

(lane 4), and heparanase from a CHO 2TT1 cell extract (lane 5) served as controls.

FIG. 27 proteolytic processing of heparanase secreted from CHO cells by trypsin. Conditioned medium of CHO cells transfected with pS1*hpa* (clone S1PPT-8) that secrete heparanase in a constitutive manner was subjected to proteolysis by trypsin. Unpurified CHO conditioned medium containing heparanase (0.5 μg heparanase per reaction) in 20 mM phosphate buffer, pH 6.8, was incubated with 0, 1.5, 15 or 150 units of trypsin for 10 minutes, at 37 °C. Reactions were stopped by transferring the reaction tubes into ice and adding 2 μg/ml aprotinin. Tryptic digest products were assayed for heparanase activity using the DMB assay.

FIG. 28a-b demonstrates proteolytic processing of p70-bac heparanase by cathepsin L. Partially purified heparanase from insect cells (10 μg) was subjected to proteolysis by 1.6 mU cathepsin L (Cat. No. 219412, Calbiochem) for 3 hours, at 30 °C, in 20 mM citrate-phosphate buffer, pH 5.4. Heparanase catalytic activity and immunoreactivity before (1) and after (2) processing with cathepsin L as were determined using the DMB heparanase activity assay and Western blot analysis with monoclonal antibody No. HP-117 (disclosed in U.S. Pat. application No. 09/071,739) followed by ECL detection (Amersham, UK), Figures 28a-b, respectively.

FIG. 29a demonstrates a hydropathy plot of SEQ ID NO:2 predicted for heparanase as calculated by the Kyte-Doolittle method for calculating hydrophilicity, using the Wisconsin University GCG DNA analysis software. I and II point at peaks of most hydrophilic regions of the enzyme.

FIG. 29b is a schematic depiction of modified heparanase species (pre-p56' and pre-p52') that contain a unique protease recognition and cleavage sequence of factor Xa - Ile-Glu-Gly-Arg↓ - or of enterokinase - Asp-Asp-Asp-Asp-Lys↓ (shaded regions, located between amino acids 119 and 120 or 157 and 158 of the heparanase enzyme depicted in SEQ ID NO:2, which acids are located within peaks I and II, respectively, of Figure 29a) which enable proteolytic processing by the respective proteases to obtain homogeneously processed and highly active heparanase species (p56' and p52', respectively).

FIG. 29c is a schematic depiction of the steps in constructing nucleic acid constructs harboring a unique protease recognition and cleavage sequence of factor Xa - Ile-Glu-Gly-Arg↓ - or of enterokinase - Asp-Asp-Asp-Asp-Lys↓.

DESCRIPTION OF THE PREFERRED EMBODIMENTS

The present invention is of genetically modified cells overexpressing recombinant heparanase and of methods for overexpressing recombinant heparanase in cellular systems, which can be used to obtain purified recombinant heparanase in large quantities. Specifically, the present invention can be used to provide a scheme for biotechnological large scale recombinant heparanase production. The invention further relates to the activation of heparanase precursors by proteolysis and further to methods of in vivo inhibition of heparanase activity.

The principles and operation of the present invention may be better understood with reference to the drawings and accompanying descriptions.

Before explaining at least one embodiment of the invention in detail, it is to be understood that the invention is not limited in its application to the details of construction and the arrangement of the components set forth in the following description or illustrated in the drawings. The invention is capable of other embodiments or of being practiced or carried out in various ways. Also, it is to be understood that the phraseology and terminology employed herein is for the purpose of description and should not be regarded as limiting.

In one aspect, the present invention provides a genetically modified cell transduced with a polynucleotide sequence encoding a polypeptide having heparanase catalytic activity, designed to direct expression of recombinant heparanase by the cell.

In another aspect, the present invention provides a method of obtaining recombinant heparanase by genetically modifying a cell with an expression vector including a polynucleotide sequence encoding a polypeptide having heparanase catalytic activity, designed to direct expression of recombinant heparanase by the cell.

As used herein in the specification and in the claims section below, the phrase "genetically modified cell" refers to a cell that includes a recombinant gene. As further detailed below the cell may be a eukaryotic or prokaryotic cell.

As used herein in the specification and in the claims section below, the term "transduced" refers to the result of a process of inserting nucleic acids into cells. The insertion may, for example, be effected by transformation, viral infection, injection, transfection, gene bombardment, electroporation or any other means effective in introducing nucleic acids into cells. Following transduction the nucleic acid is either integrated in all

or part, to the cell's genome (DNA), or remains external to the cell's genome, thereby providing stably transduced or transiently transduced cells.

As used herein in the specification and in the claims section below, the phrase "polynucleotide sequence" also means a nucleic acid sequence, typically a DNA sequence.

As used herein in the specification and in the claims section below, the term "polypeptide" also means a protein.

As used herein in the specification and in the claims section below, the phrase "heparanase catalytic activity" refers to an animal endoglycosidase hydrolyzing activity which is specific for heparin or heparan sulfate proteoglycan substrates, as opposed to the activity of bacterial enzymes (heparinase I, II and III) which degrade heparin or heparan sulfate by means of β-elimination.

As used herein in the specification and in the claims section below, the term "expression" refers to the processes executed by cells while producing and/or secreting proteins, including where applicable, but not limited to, for example, transcription, translation, folding and post translational modification and processing.

As used herein in the specification and in the claims section below, the terms "vector" and "construct" are interchangeably used herein and refer to any vehicle suitable for genetically modifying cells, including, but not limited to, viruses (e.g., bacoluvirus), phages, plasmids, phagemids, bacmids, cosmids, artificial chromosomes and the like.

As used herein in the specification and in the claims section below, the phrase "a polynucleotide sequence encoding a polypeptide having heparanase catalytic activity" refers to the potential of the polypeptide to have heparanase catalytic activity when correctly folded. Thus, this phrase refers to any catalytically active or inactive conformant of a polypeptide which may acquire at least one active conformation having heparanase catalytic activity.

According to a preferred embodiment of the present invention, the polynucleotide sequence is as set forth in SEQ ID NO:1 or a functional part thereof. The functional part encodes a polypeptide having heparanase catalytic activity. However, the scope of the present invention is not limited to SEQ ID NO:1 or a functional part thereof, as natural and man made innocuous variations thereof (e.g., mutations, such as point mutations) may also encode a protein having heparanase catalytic activity. Furthermore, it is shown hereinunder that a 52 kDa (formerly referred to as 45-50 kDa)

protein, naturally processed from a 70 kDa (formerly referred to as 60 or 60-70 kDa) protein encoded by SEQ ID NO:1, has heparanase catalytic activity. The polynucleotide sequence may be a cDNA, a genomic DNA and a composite DNA (including at least one intron derived from heparanase or any other gene) as further detailed in U.S. Pat. application No. 09/258,892, which is incorporated herein by reference. Similarly it can be derived from any animal including mammalians and avians because, as shown in U.S. Pat. application No. 09/258,892, heparanase sequences derived from species other than human beings are readily hybridizeable with the human sequence, allowing for isolation of such sequences by methods known in the art.

The functional part may be either man induced by genetic engineering or post translation artificial processing (e.g., by a protease) or naturally processed, depending on the cellular system employed.

According to another preferred embodiment of the present invention, the polypeptide includes an amino acid sequence as set forth in SEQ ID NO:2 or a functional part thereof having heparanase catalytic activity. However, the scope of the present invention is not limited to SEQ ID NO:2 or a functional part thereof, as natural and man made innocuous variations thereof (e.g., mutations, such single amino acid substitution) may also have heparanase catalytic activity. Polypeptides corresponding to species other than human and having heparanase catalytic activity are also within the scope of the present invention.

As used herein in the specification and in the claims section below, the term "functional part thereof" refers to a part of a nucleic acid sequence which encodes a polypeptide having heparanase catalytic activity or a part of a polypeptide sequence having heparanase catalytic activity.

In this context, it is important to remember that in many cases truncated or naturally processed polypeptides exhibit a catalytic activity similar to that of the natural polypeptide of the preprocessed polypeptide, respectively. Apparently, in many cases, not all of the amino acids of a protein are essential for its catalytic function, some may be responsible for other features, such as secretion, stability, interaction with other macromolecules, etc., whereas other may be replaced without affecting activity to a great extent. In many cases the processed protein exerts higher catalytic activity as compared with its unprocessed counterpart.

According to yet another preferred embodiment of the present invention, the polynucleotide sequence is selected from the group consisting of double stranded DNA, single stranded DNA and RNA.

According to still another preferred embodiment of the present invention, the cell is a bacterial cell, preferably E. *coli*.

According to a preferred embodiment of the present invention, the cell is an animal cell.

The animal cell may be a mammalian cell, such as, but not limited to, Chinese hamster ovary cell line (CHO), baby hamster kidney cells (BHK21), Namalwa cells, Dauidi cells, Raji cells, Human 293 cells, Hela cells, Ehrlich's ascites cells, Sk-Hep1 cells, $MDCK_1$ cells, $MDBK_1$ cells, Vero cells, Cos cells, CV-1 cells, NIH3T3 cells, L929 cells or BLG cells (mouse melanoma).

Alternatively, the animal cell may be a mammalian cell, such as, but not limited to, High five or Sf21.

According to another preferred embodiment of the present invention, the cell is a yeast cell, preferably a methylotrophic yeast, such as, but not limited to, *Pichia pastoris* and *Hansenula polymorpha*. Another preferred yeast is *Saccharomyces cerevisiae*.

The specified bacterial, yeast and animal cells are of specific advantage and interest since they are widely used in large scale biotechnological production of proteins and therefore knowledge has accumulated with respect to their large scale propagation, maintenance and with respect to recombinant protein purification therefrom.

According to another preferred embodiment of the present invention, the recombinant heparanase is human recombinant heparanase.

According to another preferred embodiment of the present invention, the polynucleotide sequence encodes, in addition, a signal peptide for protein secretion. The signal peptide may be the natural signal peptide of heparanase or any other suitable signal peptide, one non-limiting example is given under the Examples section hereinunder. The signal peptide sequence is fused downstream of and in frame with the heparanase sequence.

According to yet another preferred embodiment of the present invention, the method is further effected by purifying the recombinant heparanase. As further detailed hereinunder efficient purification (e.g., 90 % purified) of recombinant heparanase may be effected by a single step ion exchange (e.g., Source-S) column.

The purification may be from the cells themselves. To this end the cells are collected, e.g., by centrifugation, homogenated and the recombinant heparanase is purified from the homogenate. If the recombinant heparanase is secreted by the cells to the growth medium, then purification is preferably from the growth medium itself.

According to yet another preferred embodiment of the present invention, the method further includes a step of subjecting the cell to a substance which induces secretion into the growth medium of secretable proteins, thereby inducing secretion of the recombinant heparanase into the growth medium. Preferably, the substance is selected from the group consisting of thrombin, calcium ionophores, immune complexes, antigens and mitogens, all are known to induce secretion of native heparanase from expressing cells. As shown in the Examples section below, the calcium ionophore calcimycin (A23187) and phorbol 12-myristate 13-acetate, are effective in inducing secretion of recombinant heparanase from transduced cells into their media.

According to yet another preferred embodiment of the present invention, the cell is grown to a large biotechnological scale of at least half a liter, preferably at least 5, 7 or 35 liters of growth medium, in a bioreactor, such as but not limited to, Spinner-Basket bioreactor.

Further according to the present invention there is provided a method of purifying a recombinant heparanase from overexpressing cells or growth medium in which they grow by adsorbing the recombinant heparanase on a Source-S column under low salt conditions (e.g., about 50 mM NaCl), washing said column with low salt solution thereby eluting other proteins, and eluting the recombinant heparanase from the column by a salt gradient (e.g., 50 mM to 1 M NaCl) or a higher concentration of salt (e.g., about 0.4 M).

According to a further aspect of the present invention there is provided an antibody comprising an immunoglobulin elicited against recombinant native heparanase. The immunoglobulin therefore recognizes and binds native (i.e., non denatured) natural or recombinant heparanase.

As used herein in the specification and in the claims section below, the term "antibody" include serum immunoglobulins, polyclonal antibodies or fragments thereof or monoclonal antibodies or fragments thereof. The antibodies are preferably elicited against a surface determinant of the particulate. Monoclonal antibodies or purified fragments of the monoclonal antibodies having at least a portion of an antigen binding region, including

such as Fv, F(abl)2, Fab fragments (63), single chain antibodies (U.S. Patent 4,946,778), chimeric or humanized antibodies (64-65) and complementarily determining regions (CDR) may be prepared by conventional procedure. Purification of the serum immunoglobulins antibodies or fragments can be accomplished by a variety of methods known to those of skill including, but not limited to, precipitation by ammonium sulfate or sodium sulfate followed by dialysis against saline, ion exchange chromatography, affinity or immunoaffinity chromatography as well as gel filtration, zone electrophoresis, etc. (see 66).

According to a further aspect of the present invention there is provided an affinity substrate comprising a solid matrix and an immunoglobulin elicited against recombinant native heparanase being immobilized thereto. Methods of immobilizing immunoglobulins to solid matrices, such as cellulose, polymeric beads including magnetic beads, are well known in the art. One such method is described in the Examples section that follows. The solid support according to the present invention can be packed into an affinity column.

According to a further aspect of the present invention there is provided a method of affinity purifying heparanase. The method is effected by (a) loading a heparanase preparation on an affinity column including a solid matrix and an immunoglobulin elicited against recombinant native heparanase being immobilized thereto; (b) washing the affinity column, e.g., using low, say 0-500 mM, salt solution; and (c) eluting heparanase molecules being adsorbed on the affinity column via the immunoglobulin, e.g., using a high, say 0.5-1.5 M, salt solution.

According to a further aspect of the present invention there is provided a method of activating a heparanase enzyme comprising the step of digesting the heparanase enzyme by a protease. The heparanase enzyme according to this aspect of the present invention can be natural or recombinant, purified, partially purified or non-purified. The protease can be of any type, including, but not limited to, a cysteine protease, an aspartyl protease, a serine protease and a meatlloproteinase. Examples of specific proteases associated with the above listed protease families are provided in the Background section. The use of other proteases for which heparanase includes a recognition and cleavage sequence is envisaged. According to a preferred embodiment digesting the heparanase enzyme by the protease is effected at a pH in which the protease is active, preferably most active. It is known that some proteases are most active in acidic pH values whereas

other proteases are most active in basic pH values. The pH value at which a specific protease is most active can be readily determined by one ordinarily skilled in the art.

According to a further aspect of the present invention there is provided a method of *in vivo* inhibition of proteolytic processing of heparanase. The method according to this aspect of the present invention is effected by *in vivo* administering a protease inhibitor. The protease inhibitor can be, for example, a cysteine protease inhibitor, an aspartyl protease inhibitor, a serine protease inhibitor or a meatlloproteinase inhibitor. Examples of suitable inhibitors are provided in the Examples section that follows. Some protease inhibitors are used pharmaceutically for treatment of various conditions. *In vivo* inhibition of proteolytic processing of heparanase by a protease inhibitor can be used for treatment of cancer, metastatic cancers in particular, in which heparanase activity is involved, because, as further exemplified in the Examples section that follows, the preheparanase (non-processed, p70 heparanase) is characterized by lower activity as compared to its processed counterpart (p52 heparanase).

According to a further aspect of the present invention there is provided a nucleic acid construct comprising a first nucleic acid segment encoding for an upstream (N terminal) portion of heparanase, a second, in frame, nucleic acid sequence encoding a recognition and cleavage sequence of a protease and a third, in frame, nucleic acid sequence encoding for a downstream portion (C terminal) of heparanase, wherein the second nucleic acid sequence is in between the first nucleic acid sequence and the third nucleic acid sequence. Examples of such constructs are provided in the Examples section that follows. Preferably, the protease is selected having no recognition and cleavage sequences in the upstream and the downstream portions of heparanase, such that when expressed the modified heparanase is digested only at the introduced recognition and cleavage sequence of the protease. Preferably, the third nucleic acid sequence encodes for a catalytically active heparanase when correctly folded. However, embodiments wherein the second nucleic acid sequence is so positioned such that when expressed the modified heparanase protein is digestible into portions lacking catalytic activity are also envisaged. Such embodiments can be used to provide a heparanase species having a shorter half life, in, for example, physiological conditions, as compared with the non-modified enzyme. One ordinarily skilled in the art would know how to select

locations for introduction of the recognition and cleavage sequence such that the sequence will not hamper the catalytic activity of the enzyme prior to cleavage thereof by the protease.

The above construct, when introduced into a cell expression system can be used to provide a precursor heparanase protein comprising an upstream portion of heparanase, a mid portion of a recognition and cleavage sequence of a protease and a downstream portion of heparanase, wherein the protease is selected having no recognition and cleavage sequences in the upstream and the downstream portions of heparanase. The recognition and cleavage sequence of the protease is composed either entirely from amino acids which are not present in natural heparanase, or from amino acids which are not present in natural heparanase in part, and further from adjacent amino acids which are present in natural heparanase. Further according to the present invention there is provided a heparanase protein resulting by digesting the precursor heparanase protein described herein.

According to a further aspect of the present invention there is provided a method of obtaining a homogeneously processed, active heparanase. The method according to this aspect of the present invention is effected by (a) expressing the precursor heparanase protein in a cell which secretes the precursor heparanase protein into the growth medium to obtain a conditioned growth medium, the precursor heparanase protein including an upstream portion of heparanase, a mid portion of a recognition and cleavage sequence of a protease and a downstream portion of heparanase, wherein the protease is selected having no recognition and cleavage sequences in the upstream and the downstream portions of heparanase; (b) treating the precursor heparanase protein with the protease; and (c) purifying a proteolytic heparanase product having heparanase catalytic activity.

It will be appreciated that the various heparanase species described herein, either activated and/or precursors can be used to produce pharmaceutical compositions, including, in addition to heparanase, a pharmaceutically acceptable carrier. Affinity purified and protease treated, modified, recombinant heparanase is of particular interest for pharmaceutical applications due to its homogeneity and purity.

The present invention has advantages because it provides means for expressing, purifying and activating recombinant/natural heparanase. Such heparanase can be used in pharmaceutical compositions (see, for example, U.S. Pat. application No. 09/046,465, in which heparanase is used in the

treatment of CF), or as a source of enzyme for high throughput heparanase activity assay, which can be used for efficient screening of specific heparanase inhibitors (see, for example, U.S. Pat. application No. 09/113,168). By identifying the heparanase proteolytic activation process, novel indirect methods of *in vivo* heparanase inhibition by administration of protease inhibitors were conceived and tested *in vitro*. By identifying the heparanase proteolytic activation process, novel constructs encoding novel heparanase species has been constructed and can be used to direct the expression of a heparanase which is homogeneously processed and activated or alternatively neutralized by a dedicated protease.

EXAMPLES

Reference is now made to the following examples, which together with the above descriptions, illustrate the invention in a non-limiting fashion.

Generally, the nomenclature used herein and the laboratory procedures in recombinant DNA technology described below are those well known and commonly employed in the art. Standard techniques are used for cloning, DNA and RNA isolation, amplification and purification. Generally enzymatic reactions involving DNA ligase, DNA polymerase, restriction endonucleases and the like are performed according to the manufacturers' specifications. Similarly, standard techniques are used for the proteolysis of heparanase by various proteases. These techniques and various other techniques used while reducing the present invention to practice are generally performed according to Sambrook et al., Molecular Cloning--A Laboratory Manual, Cold Spring Harbor Laboratory, Cold Spring Harbor, N.Y. (1989), which is incorporated herein be reference. Other general references are provided throughout this document. The procedures therein are believed to be well known in the art and are provided for the convenience of the reader. All the information contained therein is incorporated herein by reference.

EXAMPLE 1

Expression of recombinant human heparanase in bacteria

Experimental Methods

Construction of expression vector: A 1.6 kb fragment of *hpa* cDNA (SEQ ID NO:1) was amplified from pfast*hpa* (*hpa* cDNA cloned in

pFastBac, see U.S. Pat. application No. 08/922,170) by PCR using specific sense primer: Hpu-550*Nde* - 5'-CGCATATGCAGGACGTCGTGG ACCTG-3' (SEQ ID NO:4) and a vector specific antisense primer: 3'pFast 5'-TATGATCCTCTAGTACTTCTCGAC-3' (SEQ ID NO:5). PCR conditions were: denaturation - 94 °C, 40 seconds, first cycle 3 minutes; annealing - 58 °C, 60 seconds; and elongation - 72 °C, 2.5 minutes, total of 5 cycles, and then denaturation - 94 °C, 40 seconds; annealing - 68 °C, 60 seconds; and elongation - 72 °C, 2.5 minutes, for additional 25 cycles.

The Hpu-550*Nde* primer introduced an *Nde*I site and an in frame ATG codon preceding nucleotide 168 of *hpa*. The PCR product was digested by *Nde*I and *Bam*HI and its sequence was confirmed with vector specific and gene specific primers, using an automated DNA sequencer (Applied Biosystems, model 373A).

A 1.3 kb *Bam*HI-*Kpn*I fragment was cut out of pFast*hpa*. The two fragments were ligated with the pRSET bacterial expression vector (Invitrogen, CA.).

The resulting plasmid, designated pRSET*hpa*S1, encoded an open reading frame of 508 amino acids (36-543, SEQ ID NO:2) of the heparanase protein, lacking the N-terminal 35 amino acids which are predicted to be a signal peptide.

Transformation: Transformation of E. *coli* BL21(DE3)pLysS cells (Stratagene) was performed following Stratagene's protocol. Briefly, using β-mercaptoethanol in the transformation buffer cells were transformed by five seconds of heat shock at 42 °C.

Expression of recombinant heparanase: E. *coli* BL21(DE3)pLysS cells transformed with the recombinant plasmid were grown at 37 °C overnight in Luria broth (LB) medium containing 100 μg/ml ampicillin and 34 μg/ml chloramphenicol. Cells were diluted 1/10 in the same medium, and the cultures were grown to an OD600 of approximately 0.5. Isopropyl-thiogalactoside (IPTG) (Promega) was added to a final concentration of 1 mM and the culture was incubated at 37 °C for 3 hours. Cells from IPTG induced cultures were cooled on ice and sedimented by centrifugation at 4,000 x *g* for 20 minutes at 4 °C, and resuspended in 0.5 ml of cold phosphate-buffered saline (PBS). Cells were lysed by sonication, and cell debris were sedimented by centrifugation at 10,000 x *g* for 20 minutes. The resulting pellet was analyzed for proteins by 10 % SDS-PAGE, essentially as described in Harlow, E. and Lane, D. Eds. in Antibodies, a laboratory manual. CSH Laboratory press. New-York.

Experimental Results

The expression of recombinant heparanase in E. *coli* BL21(DE3)pLysS cells containing the pRSET*hpa*S1 was analyzed by SDS-PAGE followed by commassie blue staining for proteins. Bacterial cells were fractionated and a protein of approximately 70 kDa, which is the expected size of the recombinant heparanase, was observed in the insoluble fraction (Figure 1, lanes 2-3). That band did not appear when negative control cells transformed with pRSET were employed (Figure 1, lane 1).

The identification of the recombinant heparanase expressed in E. *coli* was confirmed by a Western blot (data not shown) using a rabbit anti-heparanase polyclonal antibody (disclosed in U.S. Pat. application No. 09/071,739), followed by ECL detection (Amersham, UK).

As compared to known quantities of co-size separated and stained BSA, the estimated yield of the heparanase recombinant protein under the conditions described was about 0.2 mg/ml of culture (not shown). The protein was found in the insoluble fraction (inclusion bodies) and had no enzymatic activity, as was determined by the soluble ^{35}S-ECM degradation assay (not shown), however, the recombinant heparanase protein expressed in E. *coli* could provide a source for large quantities of heparanase.

It will be appreciated that solubillization and refolding of recombinant proteins expressed in E. *coli* are well known in the art (see, for example, for insulin, 70; others are reviewed in 71) and these procedures should be applied in order to obtain a functional protein having heparanase activity.

The expression of the recombinant heparanase in bacterial cells is thus demonstrated in this Example. It will be further appreciated that changes in protein length and/or amino acid composition might affect the efficiency of expression, correct folding and the potential yield of functional enzyme.

EXAMPLE 2

Expression of recombinant human heparanase in yeast

Experimental Methods

Construction of expression vectors for expression in yeast: Two expression vectors were constructed for the expression of *hpa* in *Pichia pastoris*. The first vector, designated pPIC3.5K-Sheparanase (Figure 2) contains nucleotides 63-1694 of the *hpa* sequence (SEQ ID NO:1) cloned into the expression vector pPIC3.5K (Invitrogen, CA) using a multistep procedure as follows.

A pair of primers: HPU-664I - 5'- AGGAATTCACCATGCTGCT GCGCTCGAAGCCTGCG-3' (SEQ ID NO:6) and HPL-209 5'-GAGTAGCAATTGCTCCTGGTAG-3' (SEQ ID NO:7) were used in PCR amplification to introduce an *Eco*RI site just upstream to the predicted methionine. PCR conditions were: denaturation - 94 °C, 40 seconds; annealing - 50 °C, 80 seconds; and elongation - 72 °C, 180 seconds, total of 30 cycles.

The resulting PCR product was digested with *Eco*RI and *Bam*HI and cloned into the *Eco*RI-*Bam*HI sites of the vector p*hpa*2 (described in U.S. Pat. application No. 08/922,170). The *hpa* coding region was then removed as an *Eco*RI-*Not*I fragment and cloned into the *Eco*RI-*Not*I sites of the expression vector pPIC3.5K to generate the vector pPIC3.5K-Sheparanase (Figure 2).

The second vector, designated pPIC9K-PP2 (Figure 3), includes the *hpa* coding region except for the predicted signal sequence (N-terminal 36 amino acids, see SEQ ID NO:2). The *hpa* was cloned in-frame to the α-factor prepro secretion signal in the *Pichia pastoris* expression vector pPIC9K (Invitrogen, CA). A pair of primers: HPU-559S, 5'-GTCTCGA GAAAAGACAGGACGTCGTGGACCTGGAC-3' (SEQ ID NO:8) and HPL-209 (SEQ ID NO:7, described above) were used in PCR amplification under the conditions described above.

The resulting PCR product was digested with *Xho*I and *Bam*HI and inserted into the *Xho*I-*Bam*HI sites of the vector p*hpa*2 (U.S. Pat. application No. 08/922,170).

Thereafter, the *Xho*I-*Not*I fragment containing the *hpa* sequence was removed and cloned into an intermediate vector harboring the *Sac*I-*Not*I sites of pPIC9K.

The *hpa* was removed from the later vector as a *Sac*I-*Not*I fragment and cloned into the *Sac*I-*Not*I sites of pPIC9K, thus creating the vector pPIC9K-PP2 (Figure 3).

Transformation and screening: *Pichia pastoris* strain SMD1168 (*his3*, *pep4*) (Invitrogen, CA) was used as a host for transformation. Transformation and selection were carried out as described in the Pichia expression Kit protocol (Invitrogen, CA). In all transformations the expression vectors were linearized with *Sal*I prior to their introduction into the yeast cells.

Multiple copies integration clones were selected using G-418 (Boehringer Mannheim, Germany). Following transformation the top agar

layer containing the yeast cells was removed and re-suspended in 10 ml of sterile water. Aliquots were removed and plated on YPD plates (1 % yeast extract, 2 % peptone, 2 % glucose) containing increasing concentrations of G-418 (up to 4 mg/ml). Single isolates were picked and streaked on YPD plates. G-418 resistance was then further confirmed by streaking isolates on YPD-G-418 plates.

Expression experiments: Single colonies were inoculated into 6 ml BMGY - Buffered Glycerol-complex Medium (1 % yeast extract, 2 % peptone, 100 mM potassium phosphate pH 6.0, 1.34 % yeast nitrogen base with ammonium sulfate without amino acids, 4 x 10^{-5} biotin and 1 % glycerol) and incubated at 30 °C at 250 RPM for 24 hours. Cells were harvested using clinical centrifuge and re-suspended in 2.5 ml of BMMY - Buffered Methanol-complex Medium (The same as BMGY except that 0.5 % methanol replaces the 1 % glycerol). Cells were then incubated at 30 °C at 250 RPM agitation for 48 hour. Culture supernatants were separated on SDS-PAGE and electrophoretically transferred to a nitrocellulose membrane using the Hoeffer-Pharmacia apparatus, according to manufacturer protocol. A rabbit anti-heparanase polyclonal antibody (disclosed in U.S. Pat. application No. 09/071,739) was used as a primary antibody in detection of heparanase. Horseradish peroxidase-labeled anti-rabbit antibodies and ECL Western blotting detection reagents (Amersham, UK) were used in subsequent detection steps.

Experimental Results

Both pPIC3.5K-Sheparanase and pPIC9K-PP2 *Pichia pastoris* transformants secreted a protein with a similar molecular weight of about 70 kDa, as expected for heparanase. These results indicate that the heparanase contains a signal sequence which efficiently functions as a secretion signal in *Pichia pastoris*.

G-418 resistance was used to select isolates characterized by multiple gene integration events. A faint heparanase band was observed in the supernatant of pPIC3.5K-Sheparanase transformant isolated without selection on G-418 (Figure 4, lane 1), whereas no band was observed in the corresponding position in pPIC3.5K transformant, which served as negative control (Figure 4, lane 2). A profound increase in the secretion of heparanase was observed in isolates resistance to 4 mg/ml of G-418 (Figure 4, lanes 3-6).

EXAMPLE 3

Expression and secretion of recombinant human heparanase in mammalian cells

Experimental Methods

Construction of hpa DNA expression vectors: A *hpa* gene fragment was cloned under the control of either SV40 early promoter (pS*hpa*, Figure 20a) or the CMV promoter (pC*hpa*, Figure 20e). One construct (pS*hpa*C*dhfr*, Figure 20b) also includes a selection marker, the mouse *dhfr* gene.

Specifically, a 1740 bp *hpa* gene fragment encoding for a 543 amino acid protein was introduced into pSI (Promega, USA) or pSI-C*dhfr* vectors to yield vectors pS*hpa* and pS*hpa*C*dhfr*, respectively (Figures 5a and 5b and 20a and 20b). In both cases the gene was inserted under the SV40 early promoter regulation. pS*hpa*C*dhfr* also carries an expression unit of mouse *dhfr* gene under the regulation of CMV promoter. Another plasmid, pC*dhfr* (Figure 20f), included expression unit of mouse *dhfr* gene under the regulation of CMV promoter and served as control.

A vector designed pS1*hpa* (Figure 5c, 20c) was constructed by ligating a truncated *hpa* gene fragment (nucleotides 169-1721 of SEQ ID NO:1) to a heterologous signal peptide as follows. Preprotrypsin (PPT) signal peptide (72) was generated by chemically synthesizing two complementary oligonucleotides corresponding to the signal peptide encoding DNA sequence, the first having a sequence 5'-AATTCACCATGTCTGCACTTCTGATCCTAGCTC TTGTTGGAGCTGCAGTTGCTCAGGAC-3' (SEQ ID NO:9), whereas the second having a complementary sequence 5'-CCTGAGCAACTGCAGCTC CAACAAGAGCTAGGATCAGAAGTGCAGACATGGTG-3' (SEQ ID NO:10). Annealing of the complementary oligonucleotides produced the double strand sequence encoding to the PPT signal peptide flanked by a sticky end of an *Eco*RI restriction site on the 5' end thereof and a sticky end of an *Aat*II restriction site on the 3' end thereof. Following restriction by *Eco*RI and *Aat*II of the pfast*hpa* vector, a 145 bp fragment was removed, and replaced by the 52 bp PPT DNA sequence to yield plasmid pS1*hpa*. The insert thereof was cut out with *Eco*RI and *Dot*I and ligated into the vector pSI.

A vector designed pS2*hpa* (Figure 5d and 20d) was constructed by ligating a truncated *hpa* gene fragment (nucleotides 144-1721) to the PPT signal peptide as follows. Preprotrypsin (PPT) signal peptide (72) was

generated by chemically synthesizing two complementary oligonucleotides corresponding to the signal peptide encoding DNA sequence, the first having a sequence 5'-AATTCACCATGTCTGCACTTCTGA TCCTAGCTCTTGTTGGAGCTGAGTTGC-3' (SEQ ID NO:11), whereas the second having a complementary sequence 5'-CGGCAACTGCA GCTCCAACAAGAGCTAGGATCAGAAGTGCAGACATGGTG-3' (SEQ ID NO:12). Annealing of the complementary oligonucleotides produced the double strand sequence encoding to the PPT signal peptide flanked by a stick end of an *Eco*RI restriction site on the 5' end thereof and a sticky end of a *Nar*I restriction site on the 3' end thereof.

Following restriction by *Eco*RI and *Nar*I of pS1*hpa* plasmid, a 112 bp fragment was removed therefrom and replaced by the PPT DNA sequence to give plasmid pS2*hpa* (Figure 5d, 20d).

Transfection of vectors into cells: DNA constructs were introduced into animal cells using the calcium-phosphate co-percipitaion technique essentially as described in (73).

Selection for dhfr expressing stable cellular clones: Following transfection, cells were incubated for 48 hours in a non-selective growth medium (F12 medium supplemented with 10 % fetal calf serum). Then, the medium was changed to a selection medium (DMEM supplemented with 10 % dialyzed calf serum) and cells were propagated to confluence at 37 °C, under 8 % CO_2 aeration. Methotrexate (MTX, 5000 nM) was added to the growth selection medium and resistant cellular clones were isolated. Alternatively, cells were transferred after transfection directly to a selection medium containing MTX (100 - 1000 nM).

SDS polyacrylamide gel electrophoresis and Western blot analysis: Denatured and reduced samples were loaded on ready made gradient (4-20 %) gels (Novex, USA) and separated under standard gel running conditions (as described in Protein Electrophoresis Application Guide, Hoeffer, U.S.A.). Transfer of proteins onto a PVDF membrane was performed electrophoretically by a protein transfer apparatus (Hoeffer- Pharmacia). Detection of specific protein was accomplished by a rabbit anti-heparanase polyclonal antibody (disclosed in U.S. Pat. application No. 09/071,739) (x 2000 dilution), followed by ECL detection (Amersham, UK).

Determination of heparanase activity: ECM-derived soluble HSPG assay was performed by incubating cell extracts with solubillized ^{35}S-labeled ECM (18 hours, 37 °C) in the presence of 20 mM phosphate buffer (pH 6.2), and size fractionation of the hydrolyzed fraction of the ECM by

gel filtration on a Sepharose CL-6B column. Radiolabeling of degradation fragments eluted at 0.5 < Kav < 0.8 (peak II) was determined (61).

Alternatively, degradation of soluble high molecular weight heparan sulfate or heparin molecules to smaller fragments was detected by polyacrylamide gel electrophoresis analysis. Polyacrylamide gels (7.5 %) were loaded with 2.5 mg heparin that was either untreated or incubated with heparanase containing cell extracts or media. Staining by methylen blue (74) enabled detection of the heparin molecules and its degradation products. The mobility of the molecules on the gel reflects their size. Therefore, activity of heparanase is reflected in a larger quantity of rapidly migrating heparin degradation products.

Induction of secretion: CHO stable clones and untransfected CHO cells were induced for secretion of proteins by either calcium ionophore calcimycin (A23187) (Sigma) or phorbol 12-myristate 13-acetate (PMA, Sigma), at different concentrations (0.01, 0.1 and 1.0 mg/ml), for various incubation times (2, 8, 24; 48 hours). Induction was performed in the absence of serum. Conditioned medium was collected with 10 % buffer citrate pH 5.6 and 200KIU/ml aprotinin (Protosol, Rad Chemicals, Israel), centrifuged to remove floating cells, and kept at -200 °C. The amount of secreted protein(s) was detected by Western blot analysis, and its activity was determined by ^{35}S-ECM degradation assay and soluble heparan sulfate substrate hydrolysis assay. When necessary conditioned medium was concentrated by ultrafiltration through a 10 kDa filter (Millipore).

Large scale propagation of animal cells in a Spinner-Basket bioreactor: The structure and mode of operation of the bioreactor is described in detail in reference 75. A Spinner Basket bioreactor (500 ml, New Brunswick Scientific) embedded with 10 grams of Fibracel discs (Sterillin, U.K.) was inoculated with seeding inoculum of 1.5 x 10^8 cells of a stable clone of CHO cells designated GGG_{11} that constitutively produces recombinant heparanase. Propagation of cells was performed in a medium containing 10 % serum and cell proliferation was monitored by measurement of glucose consumption.

Then growth medium was replaced with medium without serum, suitable for the production of the recombinant protein. This medium served as a source for recombinant heparanase for later purification.

Experimental Results

Expression of hpa DNA in animal cells: Expression of recombinant *hpa* gene products was detected in a human kidney fibroblasts cell line

(293), baby hamster kidney cells (BHK21) and Chinese hamster ovary (CHO *dhfr*-) cells, following transfection with the *hpa* gene (Figures 6a-b).

Analysis of recombinant heparanase by Western blotting revealed two distinct specific protein products: a large protein of about 70 kDa and a predominant protein of about 52 kDa (Figures 6a-b).

Transient expression of heparanase proteins was monitored 24 - 72 hours post transfection in various cell types.

Human fibroblasts (293 cell line) transfected with pS*hpa* (Figure 5a) or pC*hpa* constructs (Figure 5e) exhibited heparanase activity (Figure 6a, lane 4, Table 1 below).

Transfection of CHO cells with the expression vector pS*hpa*C*dhfr* (Figure 5b) and subsequent selection for MTX resistant clones resulted in the isolation of numerous clones. These cellular clones express *hpa* gene products in a constitutive and stable manner (Figure 6a, lanes 1-3).

Several CHO cellular clones have been particularly productive in expressing *hpa* proteins, as determined by protein blot analysis and by activity assays (Figures 6a, Figure 6b, lane 1, and Table 1). Although the *hpa* DNA encodes for a large 543 amino acids protein (expected molecular weight about 70 kDa) the results clearly demonstrate the existence of two proteins, one of about 70 kDa and another of about 52 kDa. These observations are similar to the results of the transient *hpa* gene expression in human 293 cells (Figure 6a, lane 4). Transient expression of pS*hpa*C*dhfr* in CHO cells revealed predominantly a 52 kDa heparanase protein (Figure 6b, lane 2).

It has been previously shown that a 52 kDa protein with heparanase activity was isolated from placenta (61) and from platelets, (62). It is thus likely that the 70 kDa protein is naturally processed in the host cell to yield the 52 kDa protein.

Heparanase secretion into the growth medium: For large scale production and purification purposes, secretion of the recombinant protein into the growth medium is highly desirable. Therefore, expression vectors were constructed (pS1*hpa* and pS2*hpa*, Figures 5c-d) that would drive translation of heparanase attached to the PPT signal peptide.

Both pS1*hpa* and pS2*hpa* plasmids directed the expression of protein product with heparanase activity in human 293 or CHO cells (Table 1). The heparanase was not secreted to the medium in CHO cells. However, transient expression of heparanase encoded by pS1*hpa* and pS2*hpa* in

human 293 cells resulted in the appearance of a single size (about 65 kDa) heparanase protein (Figure 7c, lanes 3-6).

Table 1:

Determination of Heparanase activity in transfected animal cells

Cell type	transfected DNA	Heparanase Activity
Human 293 cells	p*Chpa*	+ (a)
Human 293 cells	p*Shpa*	+ (b)
Human 293 cells	pS1*hpa*	+ (b)
Human 293 cells	pS2*hpa*	+ (b)
CHO	p*ShpaCdhfr*	+ (a)

Cell extracts were assayed for heparanase activity using ECM-derived soluble HSPG assay (a) or direct hydrolysis of soluble substrate (b). Activity detected either in transiently expressing cells (293, CHO) or stable cellular clones (CHO).

In order to induce secretion of the recombinant protein(s) into the medium, stable clones and untransfected CHO cells were induced with either calcium ionophore or PMA. The results show that induction with 1 mg/ml calcium ionophore for 2 hours stimulates the secretion of protein of about 52 kDa from stable clones but not from untransfected cells (data not shown) or untreated stable clones, while longer (24-48 hours) incubation time with 100 ng/ml of calcium ionophore induces predominantly the secretion of protein of about 70 kDa from stable clones (Figures 7a-b). The conditioned medium obtained from the treated stable clone, which exhibited the 52 kDa protein, had strong heparanase activity in ECM-derived soluble HSPG assay (Figures 8b-c), and in concentrated conditioned medium, in the gel shift assay (Figure 8a). The heparanase activity in the conditioned medium from the treated stable clone, which exhibited the 70 kDa, is lower than that of the 52 kDa fraction (Figures 8d-g), since it was active when diluted eight fold while the 70 kDa protein failed to show activity in this

dilution. It is thus possible that the 52 kDa protein is the active form of a less active pre heparanase of 70 kDa, which is naturally processed to yield the mature-active 52 kDa heparanase.

Large scale production of heparanase: Large scale propagation of heparanase expressing cells was set up in a 500 ml volume Spinner-Basket bioreactor to demonstrate the ability to obtain a dense adherent cell culture for large scale production of heparanase. Heparanase constitutively producing cell line was propagated in the Spinner- Basket bioreactor and at the end of the proliferation phase the medium was replaced with production medium which has the same composition as the growth medium but without serum. Cell proliferation and viability were constantly monitored by daily measurements of glucose concentration in the medium. Level of glucose was also the parameter used to determine the frequency of medium refreshment in the bioreactor, as described in reference 76. Results of a typical "batch run" that includes proliferation and maintenance of heparanase producing cells in a 500 ml Spinner-Basket are shown in Figure 9.

A "batch run" in a Spinner-Basket bioreactor can last about four weeks, when serum is omitted from the culture medium. The apparatus can be linearly enlarged to bioreactors of 5, 7 or 35 liters. Accordingly, larger amounts of Fibracel can be packed in those vessels and accommodate, proportionally, larger numbers of cells. The bioreactors can support cell growth for weeks, or even months, depending on the nature of the cell line and the composition of medium.

EXAMPLE 4

Expression of recombinant heparanase in virus infected insect cells: Experimental Methods

Cells: High five and Sf21 insect cell lines were maintained as monolayer cultures in SF900II-SFM medium (GibcoBRL).

Recombinant Baculovirus: Recombinant virus containing the *hpa* gene was constructed using the Bac to Bac system (GibcoBRL). The transfer vector pFastBac (see U.S. Pat. application No. 08/922,180) was digested with *Sal*I and *Not*I and ligated with a 1.7 kb fragment of p*hpa*2 digested with *Xho*I and *Not*I. The resulting plasmid was designated pFast*hpa*2. An identical plasmid designated pFast*hpa*4 was prepared as a duplicate and both independently served for further experimentations. Recombinant bacmid was generated according to the instructions of the

manufacturer with pFast*hpa*2, pFast*hpa*4 and with pFastBac. The latter served as a negative control. Recombinant bacmid DNAs were transfected into Sf21 insect cells. Five days after transfection recombinant viruses were harvested and used to infect High five insect cells, 3 x 10^6 cells in T-25 flasks. Cells were harvested 2 - 3 days after infection. 4 x 10^6 cells were centrifuged and resuspended in a reaction buffer containing 20 mM phosphate citrate buffer, 50 mM NaCl. Cells underwent three cycles of freeze and thaw and lysates were stored at -80 °C. Conditioned medium was stored at 4 °C.

Experimental Results

Degradation of soluble ECM-derived HSPG: Monolayer cultures of High five cells were infected (72 h, 28 °C) with recombinant bacoluvirus containing the pFast*hpa* plasmid or with control virus containing an insert free plasmid. The cells were harvested and lysed in heparanase reaction buffer by three cycles of freezing and thawing. The cell lysates were then incubated (18 h, 37 °C) with sulfate labeled, ECM-derived HSPG (peak I), followed by gel filtration analysis (Sepharose 6B) of the reaction mixture.

As shown in Figure 10, the substrate alone included almost entirely high molecular weight (Mr) material eluted next to V_O (peak I, fractions 5-20, Kav < 0.35). A similar elution pattern was obtained when the HSPG substrate was incubated with lysates of cells that were infected with control virus. In contrast, incubation of the HSPG substrate with lysates of cells infected with the *hpa* containing virus resulted in a complete conversion of the high Mr substrate into low Mr labeled degradation fragments (peak II, fractions 22-35, 0.5 < Kav < 0.75).

Fragments eluted in peak II were shown to be degradation products of heparan sulfate, as they were (i) 5- to 6-fold smaller than intact heparan sulfate side chains (Kav approx. 0.33) released from ECM by treatment with either alkaline borohydride or papain; and (ii) resistant to further digestion with papain or chondroitinase ABC, and susceptible to deamination by nitrous acid. Similar results (not shown) were obtained with Sf21 cells. Again, heparanase activity was detected in cells infected with the *hpa* containing virus (pF*hpa*), but not with control virus (pF). This result was obtained with two independently generated recombinant viruses. Lysates of control not infected High five cells failed to degrade the HSPG substrate.

In subsequent experiments, the labeled HSPG substrate was incubated with medium conditioned by infected High five or Sf21 cells.

As shown in Figures 11a-b, heparanase activity, reflected by the conversion of the high Mr peak I substrate into the low Mr peak II which represents HS degradation fragments, was found in the growth medium of cells infected with the pF*hpa*2 or pF*hpa*4 viruses, but not with the control pF1 or pF2 viruses. No heparanase activity was detected in the growth medium of control non-infected High five or Sf21 cells.

The medium of cells infected with the pF*hpa*4 virus was passed through a 50 kDa cut off membrane to obtain a crude estimation of the molecular weight of the recombinant heparanase enzyme. As demonstrated in Figure 12, all the enzymatic activity was retained in the upper compartment and there was no activity in the flow through (<50 kDa) material. This result is consistent with the expected molecular weight of the *hpa* gene product.

In order to further characterize the *hpa* product the competition effect of heparin, additional substrate of heparanase was examined.

As demonstrated in Figures 13a-b, conversion of the peak I substrate into peak II HS degradation fragments was completely abolished in the presence of heparin.

Altogether, these results indicate that the heparanase enzyme is expressed in an active form by insect cells infected with Baculovirus containing the newly identified human *hpa* gene.

Degradation of HSPG in intact ECM: Next, the ability of intact infected insect cells to degrade HS in intact, naturally produced ECM was investigated. For this purpose, High five or Sf21 cells were seeded on metabolically sulfate labeled ECM followed by infection (48 h, 28 °C) with either the pF*hpa*4 or control pF2 viruses. The pH of the medium was then adjusted to pH 6.2-6.4 and the cells further incubated with the labeled ECM for another 48 h at 28 °C or 24 h at 37 °C. Sulfate labeled material released into the incubation medium was analyzed by gel filtration on Sepharose 6B.

As shown in Figures 14a-b and 15a-b, incubation of the ECM with cells infected with the control pF2 virus resulted in a constant release of labeled material that consisted almost entirely (>90%) of high Mr fragments (peak I) eluted with or next to V_O. It was previously shown that a proteolytic activity residing in the ECM itself and/or expressed by cells is responsible for release of the high Mr material. This nearly intact HSPG provides a soluble substrate for subsequent degradation by heparanase, as also indicated by the relatively large amount of peak I material accumulating when the heparanase enzyme is inhibited by heparin (Figure

17). On the other hand, incubation of the labeled ECM with cells infected with the pF*hpa*4 virus resulted in release of 60-70% of the ECM-associated radioactivity in the form of low Mr sulfate-labeled fragments (peak II, 0.5 <Kav< 0.75), regardless of whether the infected cells were incubated with the ECM at 28 °C or 37 °C. Control intact non-infected Sf21 or High five cells failed to degrade the ECM HS side chains.

In subsequent experiments, as demonstrated in Figures 16a-b, High five and Sf21 cells were infected (96 h, 28 °C) with pF*hpa*4 or control pF1 viruses and the growth medium incubated with sulfate-labeled ECM. Low Mr HS degradation fragments were released from the ECM only upon incubation with medium conditioned by pF*hpa*4 infected cells. As shown in Figure 17, production of these fragments was abolished in the presence of heparin, due to its competitory nature. No heparanase activity was detected in the growth medium of control, non-infected cells. These results indicate that the heparanase enzyme expressed by cells infected with the pF*hpa*4 virus is capable of degrading HS when complexed to other macromolecular constituents (i.e. fibronectin, laminin, collagen) of a naturally produced intact ECM, in a manner similar to that reported for highly metastatic tumor cells or activated cells of the immune system.

Thus, insect cells of several origins (such as Sf21 from *Spodoptera frugiperda* and High five from *Trichoplusia ni*) may be infected productively with baculovirus. Insect cells are infected with recombinant baculovirus in which viral DNA sequences have been replaced with DNA sequences coding for a protein of interest. The protein of interest is expressed during the very late phase of infection. A major advantage of the baculovirus expression system is that it can be used for expressing large amounts of recombinant protein compared to other popular expression systems in eukaryotes (e.g., expression in CHO cells). Another advantage of the system is that insect cells have most of the protein processing capabilities of higher eukaryotic cells. Thus, proteins produced in the recombinant baculovirus-infected cells can undergo co-and post translational processing yielding proteins which are similar to the natural protein.

Scaling up the process of culturing and infecting insect cells with baculovirus is required for the production of recombinant protein of choice, in milligram and up to gram quantities. These quantities may be required for both research or commercial use. Scaling up the process involves a

variety of fields, such as medium development, metabolic studies, protein purification and quantification.

Several problems are inherent to this system and effect the process of scaling up. Upon infection, insect cells become increasingly fragile and sensitive to the physiochemical environment of the culture. One of the primary goals of the bioengineer is to oxygenate large scale, high-density culture sufficiently, at low shearing rates. Although oxygen uptake rates of insect cells are similar to mammalian cell lines, it was found that after infection oxygen uptake rates doubles. An optimization process, aimed for setting-up of bioreactor parameters is required, for supplying oxygen to the cells without damaging them.

The spinner Bellco, Cat. 1965-56001 was used for scaling up as described. This is a double-wall type spinner. Temperature was controlled by water circulated from a 12 liter water bath (Fried Electric, Model TEP1) equipped with a heater and a thermostat. The spinner was aerated with both air, using an aquarium pump (Rena 301) and oxygen. An oxygen cylinder (medical grade) was connected to the spinner through a two stage regulator set to a pressure of 2 *psi*. Both air and oxygen were connected to the spinner through a T-connector equipped with valves that enabled a control over the flow rates of air and of oxygen. A tubing for delivering air mixed with oxygen was connected to the sparger of the spinner through a 0.2μ-size filter. The sparger used was of an open type, releasing air-oxygen mixture through an orifice of 3 mm inner diameter. The stirring function was provided by a low-RPM magnetic stirrer (LH, type 20, LH fermentation Co.), placed beneath the spinner.

High five and Sf21 cells were used alternatively for large scale production of heparanase. Cell culture was gradually built up to $1.2x10^{10}$ cells. Eight shake flasks of 500 ml-size were used for culturing cells to $3x10^6$ cells/ml. Cells were cultured with protein-free medium (Insect-Xpress, Bio Whittaker). 1.5 liters of the above culture was used for seeding a 6 liters-size spinner. At the time of seeding, culture was diluted to 3 liters with fresh medium. Air was sparged into the culture at 0.5 liters/min. Stirring rate was 50 RPM and temperature was set to 28 °C. Two days after seeding, culture volume was doubled again, from 3 liters to 6 liters. Cell density was adjusted at that time to $1x10^6$ cells/ml. At that time pure oxygen was sparged at 1.5 liters/min in addition to the sparging of air (at 0.5 liters/minute).

Infection of the culture took place one day after doubling the culture volume from 3 liters to 6 liters, as described. Cells were counted and infected with the heparanase-coding recombinant virus pF*hpa2* at a multiplicity of infection (MOI) of 0.1 or 1.0. The infected culture was maintained for approximately 72 hours under conditions set for 6 liters-size culture: Oxygen 1.5 liters/min, air 0.5 liters/min, temperature 28 °C, agitation at 50 RPM.

Viability of cells in culture was tested every 4 hours, starting from 62 hours after virus infection and on. Viability of cells was determined by staining cells with Trypan Blue dye. The culture was harvested when viability reached 70-80 %. Cells and cell debris were removed by centrifugation (IEC B-22M, Rotor Cat. 878, 20 min. at 4 °]C at 7,000 RPM). Supernatants were filtered through 0.2μ size cartridge (Millipore, Cat. KV0304HB3). Virus and small-size debris were removed with a 300 kDa-size cross-flow cartridge (Millipore, Cat. CDUF006LM). Heparanase was concentrated from filtrate obtained from the 300 kDa-size cartridge with 10 kDa size cross-flow cartridge (Millipore, Cat. SK1P003W4). The final concentrated solution had a volume of between 0.5 liters and 1 liters. Heparanase was purified from the concentrated solution on HPLC. Table 2 below summarizes the results of two large scale heparanase production by insect cells experiments.

TABLE 2

Batch No.	Cells used	MOI used	Volume of culture (L)	Harvest time post infection (hours)	Cell viability at harvest (%	heparanase in harvest (mg/ml)
30	Sf21	0.1	4.5	78	76	0.44
31	Hi-5	0.1	6.0	75	76	0.16

EXAMPLE 5

Purification of recombinant heparanase

Experimental Methods and Results

Methods and Results: Baculovirus infected insect cells (1 or 5 liter of High five cell suspension) were harvested by centrifugation. The supernatant was passed through 0.2 micron filter (Millipore), then filtered through 300K cartridge (Millipore). The <300 kDa retentate (about 300 ml) was washed by further filtration with 2 volumes of phosphate buffered saline (PBS). The <300 kDa filtrate was then concentrated by 10K cellulose cartridge (Millipore). The >10 kDa retentate was diluted three fold with 10 mM phosphate buffer pH 6.8 to prepare for applying the crude enzyme preparation onto a Source-S column (Pharmacia).

The diluted >10 kDa retentate was subjected to a Source-S column (2.5 x 10 cm) pre equilibrated with 10 mM phosphate buffer pH 6.8, 50 mM NaCl). Most of the contaminating proteins did not bind to the column while heparanase bound tightly. Heparanase activity was eluted by a linear gradient of 0.05 M NaCl - 1 M NaCl in phosphate buffer pH 6.8 and fractions of 5 ml were collected.

The fractions having the highest activity in degrading sulfate labeled ECM were combined. The 0.4 M NaCl fractions were about 90 % pure and exhibited the highest activity (Figure 18, lane 9). A rabbit anti-heparanase polyclonal antibody detected the purified enzyme in Western blot - ECL analysis (Figure 19, lane 9).

These results demonstrate a powerful single step purification of recombinant heparanase from culture supernatants. Obviously, other purification methods, such as affinity purification using, for example, solid support bound heparanase substrates, heparanase inhibitors or anti-heparanase antibodies, size exclusion, hydrophobic interactions, etc. can be additionally employed.

EXAMPLE 6

Purification of heparanase and production of highly active heparanase species by proteolytic processing

Experimental Methods

Construction of *hpa* DNA expression vectors, transfection thereof into cells, selection for *dhfr* expressing stable cellular clones, induction of secretion and SDS polyacrylamide gel electrophoresis and Western blot analyses were all performed as described hereinabove under Example 3.

Heparanase activity using DMB assay: For each sample, 100 µl heparin sepharose (50 % suspension in 1 x buffer A - containing 20 mM Phosphate citrate buffer pH 5.4, 1 mM $CaCl_2$ and 1 mM NaCl) were incubated in 0.5 ml eppendorf tube for 17 hours with a tested enzyme preparation. At the end of the incubation period, samples were centrifuged for 2 minutes at 1000 rpm and the supernatants were analyzed for sulfated polyanions (heparin) using the colorimetric dimethylmethylene blue assay as follows.

Supernatants (100 µl) were transferred to plastic cuvettes and diluted to 0.5 ml with PBS supplemented with 1 % BSA. 1,9-Dimethylmethylene blue (32 mg dissolved in 5 ml ethanol and diluted to 1 liter with formate buffer) (0.5 ml) was added to each cuvette. Absorbency at 530 nm was determined using a spectrophotometer (Cary 100, Varian). For each sample a control, to which the enzyme was added at the end of the incubation period, was included. For further details, see U.S. Pat. No. 09/113,168, which is incorporated by reference as if fully set forth herein.

Heparanase activity using the tetrazolium assay: Heparanase activity was determined in reactions containing buffer A and 50 µg heparan sulfate in a final volume of 100 µl. Reactions were performed in a 96 well microtiterplate at 37 °C for 17 hours. Reaction were thereafter stopped by the addition of 100 µl tetrazolium blue reagent (0.1 % tetrazolium blue in 0.1 M NaOH) to each well. Color was developed following incubation at 60 °C for 40 minutes. Color intensity was quantitatively determined at 580 nm using a microtiterplate reader (Dynatech). For each sample a control, to which the enzyme was added at the end of the incubation period, was included. A glucose standard curve of 1-15 µg glucose was included in each assay. Heparanase activity was calculated as ΔO.D. of the sample containing the substrate minus the O.D of the control sample. The result was converted to µg glucose equivalent. One unit is defined as µg glucose equivalent produced per minute. For further details, see U.S. Pat. No. 09/113,168, which is incorporated by reference as if fully set forth herein.

Production of rabbit anti-native heparanase polyclonal antibodies: Rabbits were immunized in three two weeks intervals with 200 mg of purified human recombinant heparanase protein produced in baculovirus infected Sf21 insect cells (see Examples 4-5 above) emulsified with an equal volume of complete Freund's adjuvant. Ten days after the third immunization rabbits were bled and serum was examined for reactivity with recombinant heparanase. Four weeks after bleeding another boost was injected and 10 days later blood was collected.

Purification of heparanase from mammalian cell extract using ion exchange chromatography: 2TT1 CHO cells (2 x 10^8 cells stably transfected with p*ShpaCdhfr*, Figure 20b) were extracted in 2.5 ml of 10 mM phosphate citrate buffer, pH 5.4. The extract was centrifuged at 2,750 x g for 5 minutes and the supernatant was collected for heparanase enzyme purification using cation exchange chromatography as follows. An HPLC column (mono-S HR 5/5, Pharmacia Biotech) was equilibrated with 20 mM sodium phosphate buffer, pH 6.8, and the supernatant was loaded thereon. Proteins were eluted from the column using a linear gradient of 0 to 1 M sodium chloride in 20 mM sodium phosphate buffer, pH 6.8. The gradient was carried out in 20 column volumes at a flow rate of one ml per minute. Elution of proteins was monitored at 214 nm (Figure 23a) and fractions of 1 ml each were collected. An aliquot from each fraction was analyzed for heparanase activity using the DMB assay and for immunoreactivity using a mouse anti-heparanase monoclonal antibody (see U.S. Pat. No. 09/071,739, which is incorporated herein by reference). Most of the heparanase was eluted in fractions 19-20.

Preparation of an affinity column with anti-native heparanase antibodies: An affinity column was prepared using the Immunopure Protein G IgG Orientation Kit (Pierce). To this end, 17 mg of the above described rabbit anti-native heparanase polyclonal antibody, purified on protein G sepharose, were bound to a column containing 2 ml Immunopure immobilized protein G. The antibody was cross linked to the protein G with DMP. Unreacted imidate groups were blocked and the column was equilibrated with 20 mM phosphate buffer, pH 6.8.

Purification of heparanase using the affinity column: 0.5 x 10^8 2TT1 CHO cells were suspended in 2.5 ml of 20 mM phosphate citrate buffer, pH 5.4. Cells were frozen in liquid nitrogen and subsequently thawed at 37 °C. Freezing and thawing were repeated two more times. The extract was then centrifuged for 15 minutes at 4000 g and the resulting

supernatant was loaded onto the affinity column and was incubated, to allow binding of the enzyme to the column, at 4 °C for 17 hours under head-over-tail shaking. Thereafter, unbound proteins were washed until absorbency at 280 nm reached zero. Proteins were eluted from the column with 0.1 M glycine HCl buffer, pH 3.5. 900 µl fractions were collected into eppendorf tubes each containing 100 µl of 1 M phosphate buffer, pH 8. The presence of heparanase in the eluted fractions was determined by Western blotting following gradient 4-20 % SDS-PAGE of 20 µl samples using anti-heparanase monoclonal antibody (see U.S. Pat. No. 09/071,739). Heparanase activity was determined in 30 µl samples using the above described DMB assay.

Construction of heparanase expression vectors with a unique protease cleavage sequence: Expression vectors for the production of a heparanase protein species carrying a unique proteolytic cleavage site were designed and constructed. Two independent sites, just upstream of amino acids 120 or 158 (SEQ ID NO:2), both are peaking on the hydropathy plot, as calculated by the Kyte-Doolittle method for calculating hydrophilicity, using the Wisconsin University GCG DNA analysis software (Figure 29a), were selected for insertion of either one of two protease recognition and cleavage sequences within the *hpa* cDNA sequence to yield two heparanase species designated herein as pre-p56' and pre-p52', which, following digestion with their respective protease, yield truncated proteins designated herein p52' and p56', respectively. A first sequence included 4 amino acids (Ile-Glu-Gly-Arg↓, SEQ ID NO:13) which constitute a factor Xa recognition and cleavage sequence. An alternative, second, sequence included 5 amino acids (Asp-Asp-Asp-Asp-Lys↓, SEQ ID NO:14) which constitute a enterokinase recognition and cleavage sequence. These sequences do not appear in the natural enzyme (SEQ ID NO:2).

To this end, the following PCR primers were constructed:

52-Xa - 5'-CCATCGATAGAAGGACGAAAAAAGTTCAAGAACAGCACCTAC-3' (SEQ ID NO:15); 52x-Cla - 5'-GGATCGATTGGTAGTGTTCTCGGAGTAG-3' (SEQ ID NO:16); 56-Xa - 5'-GGATCGATAGAAGGACGATCTCAAGTCAACCAGGATATT-3' (SEQ ID NO:17); 56x-Cla - 5'-CCATCGATGCCCAGTAACTTCTCTCTTCAAAG-3' (SEQ ID NO:18); hpl 967 - 5'-TCAGATGCAAGCAGCAACTTTGGC-3' (SEQ ID NO:19); hpu 685 - 5'-GAGCAGCCAGGTGAGCCCAAGAT-3' (SEQ ID NO:20); 52-EK 5'-CCATCGATGACGACGACAAGAAAAAGTTCAAGAACAGCACCTAC-3' (SEQ ID NO:21); 52e-Cla - 5'-

GGATCGATCTGGTAGTGTTCTCGGAGTAG-3' (SEQ ID NO:22); 56-EK - 5'-GGATCGATGACGACGACAAGTCTCAAGTCAACCAGGAT ATTTG-3' (SEQ ID NO:23); and 56e-Cla - 5'-CCATCG ATTTGGGAGTAACTTCTCTCTTCAAAG-3' (SEQ ID NO:24).

The following constructs were prepared (Figure 29b):

(i) Construction of pre-p52'-Xa *hpa* in pFast: A first PCR reaction was performed with a pFast*hpa2* template and with primers 52-Xa and hpl 967. The resulted 1180 bp fragment was digested with *Cla*I and *Afl*II and a 220 bp fragment was isolated. A second PCR reaction was performed with a pFast*hpa2* template and with primers 52x-Cla and hpu 685. The resulting 500 bp fragment was digested with *Cla*I and *Aat*II and a 370 bp fragment was isolated. The *Cla*I-*Afl*II 220 bp and the *Cla*I-*Aat*II 370 bp fragments were ligated to a 5,900 *Aat*II-*Afl*II fragment of the pFast*hpa2* plasmid.

(ii) Construction of pre-p56'-Xa *hpa* in pFast: A first PCR reaction was performed with a pFast*hpa2* template and with primers 56-Xa and hpl 967. The resulted 1290 bp fragment was digested with *Cla*I and *Afl*II and a 340 bp fragment was isolated. A second PCR reaction was performed with a pFast*hpa2* template and with primers 56x-Cla and hpu 685. The resulting 380 bp fragment was digested with *Cla*I and *Aat*II and a 250 bp fragment was isolated. The *Cla*I-*Afl*II 340 bp and the *Cla*I-*Aat*II 250 bp fragments were ligated to a 5,900 *Aat*II-*Afl*II fragment of the pFast*hpa2* plasmid.

(iii) Construction of pre-p52'-Enterokinase *hpa* in pFast: A first PCR reaction was performed with a pFast*hpa2* template and with primers 52-EK and hpl 967. The resulted 1180 bp fragment was digested with *Cla*I and *Afl*II and a 220 bp fragment was isolated. A second PCR reaction was performed with a pFast*hpa2* template and with primers 52e-Cla and hpu 685. The resulting 500 bp fragment was digested with *Cla*I and *Aat*II and a 370 bp fragment was isolated. The *Cla*I-*Afl*II 220 bp and the *Cla*I-*Aat*II 370 bp fragments were ligated to a 5,900 *Aat*II-*Afl*II fragment of the pFast*hpa2* plasmid.

(iv) Construction of pre-p56'-Enterokinase *hpa* in pFast: A first PCR reaction was performed with a pFast*hpa2* template and with primers 56-EK and hpl 967. The resulted 1290 bp fragment was digested with *Cla*I and *Afl*II and a 340 bp fragment was isolated. A second PCR reaction was performed with a pFast*hpa2* template and with primers 56e-Cla and hpu 685. The resulting 380 bp fragment was digested with *Cla*I and *Aat*II and a

250 bp fragment was isolated. The *Cla*I-*Afl*II 340 bp and the *Cla*I-*Aat*II 250 bp fragments were ligated to a 5,900 *Aat*II-*Afl*II fragment of the pFast*hpa*2 plasmid.

Construction of plasmids for expression of heparanase with protease digestion sequence: Each one of the four constructs (i to iv) described hereinabove includes an *Aat*II-*Afl*II fragment which includes a factor Xa or enterokinase recognition and cleavage sequence positioned at one of the described alternative sites, i.e., upstream amino acids 120 or 158 (SEQ ID NO:2). The *hpa* constructs described in Figures 5a-e and 20 a-e, as well as the pFast*hpa* constructs, each includes a single *Aat*II site and a single *Afl*II site within the *hpa* cDNA sequence, thus enabling the insertion by replacement of the 220 or 340 *Aat*II-*Afl*II fragments as desired.

Experimental Results

Expression of hpa DNA in animal cells: As already shown and discussed under Example 3 above, in order to drive transient or stable expression of the *hpa* gene in animal cells, the *hpa* gene was cloned into expression vectors, where transcription is regulated by promoters of viral origin (SV40, CMV) to ensure efficient transcription (Figure 5a-e). All vectors were suitable for transient expression of *hpa* in animal cells, but only vectors that include an expression cassette for the mouse *dhfr* gene (Figures 5b and 20f, the latter serves as a negative control) could be subjected to selection by mrthotrexate (MTX). Selection enables the establishment of cell lines that constitutively produce high levels of recombinant heparanase.

Cell lines of different origins have been transfected and expressed human heparanase gene: Transient expression of recombinant heparanase was detected in a human kidney fibroblasts cell line 293 (Figure 6a), baby hamster kidney cells (BHK21; Figure 21a) and Chinese hamster ovary cells (CHO; Figure 6b). Stable expression of heparanase in CHO cells is shown in Figures 6a-b.

Transfection of CHO cells with the expression vector pS*hpa*C*dhfr* (Figure 5b) or co-transfection with pS1*hpa* and p*Cdhfr* (Figure 5c and 20f), followed by selection for MTX resistant clones resulted in the isolation of numerous clones. These cellular clones express *hpa* gene products in a constitutive and stable manner (Figure 6a, lanes 1-3).

Analysis of expression of recombinant heparanase in mammalian cells revealed two distinct specific protein products: a large protein of about

70 kDa (which is referred to herein as p70) and a predominant protein of about 50 kDa, which is referred to herein as p52 (Figures 6a, 21a).

Although the *hpa* DNA encodes a large 543 amino acids protein (expected molecular weight about 61 kDa), the results clearly demonstrate the existence of two proteins. These observations are similar to the results of the transient *hpa* gene expression in human 293 cells (Figure 6a, lane 4). BHK21 cells, transiently transfected with pS1*hpa* (Figure 5c) express predominantly the p52 form of recombinant heparanase (Figure 21a, lane 1 marked by an arrow). Stable CHO clones express predominantly the p52 protein (Figure 6b, lane 2).

The presence of both p70 and p52 heparanase was detected in all cells that expressed the *hpa* gene, although the relative concentrations of the proteins varied between different cell types.

Cells transfected with pS1*hpa* (Figure 5c) expressed p52 (Figure 21a) indicating that the replacement of the putative heparanase signal peptide by the PPT signal sequence did not affect the expression and processing of the protein.

All cell extracts exhibited high heparanase activity following the introduction of the *hpa* gene. Human. 293 cells transfected with pS*hpa* (Figure 5e) exhibited high heparanase activity (Figure 21b).

It has been previously shown that a 52 kDa protein with heparanase activity was isolated from placenta (61) an platelets (62).

It is thus concluded that the p70 protein is a preheparanase that is naturally processed in the host cell to yield the p52 protein.

Heparanase secretion into the growth medium: For large scale production and purification purposes, secretion of the recombinant protein into the growth medium is highly desirable. Therefore, expression vectors were constructed (pS1*hpa* and pS2*hpa*, Figures 5c-d) to direct translation of heparanase attached to the PPT signal peptide, a secretion signal peptide.

Both pS1*hpa* and pS2*hpa* plasmids directed the expression of protein product with heparanase activity in human 293 or CHO cells (Figures 7c, 22a-b). Transient expression of heparanase from pS1*hpa* and pS2*hpa* resulted in the appearance of a single size (about 70 kDa) heparanase protein in the medium (Figure 7c, lanes 3-6), similar to the larger form of recombinant heparanase detected in the cells.

CHO cells, stably transfected with either pS*hpa*C*dhfr* (2TT1 clones) or pS1*hpa* (S1PPT clones) were further subcloned to yield stable clones which maintain their genetic and cellular characteristics stability in the

absence of MTX selection. To this end, the limiting dilution procedure was employed, in which cells were cloned under non-selective conditions and clones exhibiting the above stability were selected for further analysis.

2TT1 and S1PPT clones under (clones 2TT1 and S1PPT-p) or after (clones 2TT1-2, 2TT1-8, S1PPT-4 and S1PPT-8) selection with high MTX yielded stable clones exhibiting moderate (clones 2TT1 (Figure 22b), 2TT1-2, 2TT1-8) or high (clones S1PPT-p, S1PPT-4, S1PPT-8 (Figure 22a)) constitutive secretion of heparanase into the growth medium. The secreted protein was of about 70 kDa, similar to p70, the larger heparanase form found within the cells (Figures 22a-b). Only when a large amount of p70 protein are found in the medium, a residual amount of the smaller heparanase form, p52, could be detected (Figure 22a, lane 4).

In the conditioned medium containing heparanase, some heparanase activity could be detected, although not as high as the activity measured in the respective cell extracts which, as determined immunologically, have comparable heparanase concentrations. Some improvement in secretion could be detected by calcium ionophore treatment, but the effect was transient (Figure 22a, lane 4).

The purification of recombinant heparanase from 2TT1 CHO cells by ion exchange chromatography: Clone 2TT1-8 was used for large scale production of heparanase. In this cell line, the p52 form of heparanase is predominantly expressed within the cells. The cells are grown adherent to the tissue culture flask surface and were harvested when the cell culture reaches confluency.

Purification of a non-abundant protein from cells is a challenging task, where only an carefully designed and accurately discriminating protocol enables purification. See U.S. patent No. 5,362,641 and references 61 and 62 describing the purification of heparanase from placenta and platelets.

Here, a cation exchange chromatography procedure was selected for purification based on successful use thereof in the purification of insect cells produced recombinant heparanase, as described in Example 5 hereinabove.

Separation of the total protein content of 2TT1-8 cell extract on a mono-S cation exchange column is shown in Figure 23a. The vast majority of cellular proteins were eluted from the column prior to the elution of heparanase (Figure 23b). It is important to note that the p52 and the p70 were co-eluted under these conditions. Furthermore, a tight correlation was

found between the presence of heparanase, as detected immunologically (Figure 23b), and its activity, as measured by the DMB (Figure 23c) and the tetrazolium (Figure 23d) activity assays.

Thus, using the above described purification protocol, one obtains ample amounts of highly active and purified heparanase which is highly suitable for use in a high throughput screening assay for heparanase activity, e.g., in the presence of candidate heparanase inhibitors, for example, combinatorial inhibitor libraries. Further details relating to a heparanase high throughput assay are provided in U.S. Pat. application No. 09/113,168, which is incorporated herein by reference.

The purification of heparanase by an anti-heparanse affinity column: Partially purified, active recombinant heparanse produced in SF21 insect cells infected with a baculovirus containing the *hpa* cDNA, was used to immunize rabbits for the production of polyclonal antibodies against the native recombinant heparanase protein. This antibody was thereafter purified and was used to construct a heparanase affinity column.

Cellular extract of CHO 2TT1-8 cells was loaded on the column for affinity separation. Figure 24a-b clearly show that heparanase was specifically and efficiently bound to the affinity column. Moreover, high salt elution of the bound heparanase from the column was efficient and the activity of the eluted heparanase (Figure 24b) was tightly correlated with the presence of the recombinant enzyme (Figure 24a). Thus, using an affinity column as herein described, one can obtain a highly purified and highly active recombinant or natural heparanase in single step purification, which can be used in pharmaceutical applications. Furthermore, combining the Mono-S and affinity columns into a two step purification procedure, will ensure even better results in terms of both purification and yield.

In addition, the tetrazolium assay is based on the detection of free reducing sugar ends. As such it requires heparanase preparations devoid of such reducing ends. Heparanase purified using the above described affinity column is devoid of such reducing ends, and is therefore highly applicable for the tetrazolium activity assay.

Proteolytic processing of heparanase by protease from insect cells: Production of human recombinant heparanase in insect cells (Sf21), via baculovirus infection, and the subsequent purification of that protein are described in U.S. Pat. Nos. 08/922,170; 09/071,618; 09/109,386; and in PCT/US98/17954, all of which are incorporated herein by reference.

Briefly, conditioned medium of Sf21 cells that were infected with recombinant baculovirus, secrete heparanase to the medium. This heparanase is a glycosylated protein with an apparent molecular weight of 70 kDa. The size of that protein is similar to the p70 produced by mammalian cells, and it possesses limited heparanase activity. This heparanase protein is referred to herein as p70-bac heparanase.

Purification of p70-bac heparanase from insect cells conditioned medium involved sequential filtration steps and a cation exchange column (Source-S). Fractions that contain predominantly p70-bac heparanase protein are collected. This purification protocol and results are described hereinabove.

The effect of different pH values on the activity and intactness of p70-bac heparanase was examined in an attempt to establish a pH optimum for heparanase activity. It was found that exposure of p70-bac heparanase to pH 4.0 for one week at 4 °C resulted in significant (seven fold) increase in activity (Figure 25b). This activation was protease dependent as is evident form the inhibition of activation caused by a protease inhibitors cocktail (Figure 25b).

The fate of the p70-bac heparanase following exposure to acidic pH was uncovered by Western-blot analysis (Figure 25a). Following exposure to pH 4, p70-bac heparanase was converted into a lower molecular weight form, of about 56 kDa, which is referred to herein as p56 (Figure 25a, lane C). Proteolysis was inhibited in the presence of protease inhibitors (Figure 25a, lane B).

This is the first record demonstrating (i) *in vitro* proteolytic processing of recombinant heparanase, (ii) associated with a significant increase in heparanase activity.

To further characterize the protease(s) involved in processing and activation of p70-bac heparanase, a collection of individual protease inhibitors was employed (Figures 25c-d). The inhibitors antipain, E-64, leupeptin and chemostatin were most effective in preventing the activation of p70-bac heparanase at low pH. The effect was due to inhibition of the proteolytic processing of the p70-bac heparanase as is evident from the Western blot analysis of Figure 25c. Antipain and leupeptin are known to inhibit serine and cysteine proteases, while E-64 inhibits only cysteine proteases. These results therefore indicate that a cysteine protease(s) present in the conditioned medium of insect cells are responsible for the

activation of p70-bac heparanase, by processing the enzyme into a lower and more active p56 molecular weight form.

N-terminal sequencing of gel separated and PVDF transferred p56 heparanase revealed the sequence Ser-Gln-Val-Asn-Gln (SEQ ID NO:25), which corresponds to a new heparanase species that starts at Ser 120 of the full length enzyme (SEQ ID NO:2).

Proteolytic processing of heparanase by trypsin and cathepsin L: The activation of p70-bac heparanase by protease(s) from insect cells conditioned medium could be reproduced by mild digestion with trypsin (Figures 26a-b). Trypsin, 1.5 to 500 units per 10 μg p70-bac heparanase, gradually activated the protein, reaching maximal activation of five-fold already at 15 units trypsin (Figure 26a). Activation of p70-bac heparanase correlated with the expected cleavage of a portion of the p70-bac heparanase into smaller heparanase species, of about 56 kDa (Figure 26b). Smaller fragments of heparanase were also obtained by trypsinization (Figure 26b, lanes 2-3).

Similarly, recombinant heparanase processing and activation occurred when mild trypsin digestion was employed on a crude conditioned medium of CHO cells that secrete mammalian p70 heparanase (Figure 27). Activation was dose dependent.

Processing and activation of recombinant CHO produced and secreted heparanase (p70) was also obtained by mild treatment with Cathepsin L, which is a known cysteine protease (Figures 28a-b). Processing by this protease resulted in several digestion products, of about 56, 34 and 21 kDa (Figure 28b, lane 2).

It is shown herein that proteolytic digestion of recombinant heparanase from a variety of sources and by a variety of proteases results in (i) processing of the enzyme into a lower molecular weigh species; and (ii) increased catalytic activity. Processing and activation of heparanase in a similar fashion is anticipated to take place *in vivo* as well and therefore *in vivo* inhibition of proteases can be used to indirectly inhibit heparanase processing and activation.

Design of expression vectors to express heparanase precursor species adapted for in vitro activation by proteases: The p52 heparanase protein (as characterized in CHO, 293 and BHK21 cells, placental and platelets heparanase) and the p56 heparanase protein (as characterized after processing of the p70-bac heparanase) are presently the forms of heparanase that exhibit the highest enzymatic activity. It is shown herein

that these heparanase species are the result of proteolytic cleavages of heparanase. As was determined by solid phase microsequencing the cleavage site of p70-bac heparanase is effected between amino acids 119 and 120 (SEQ ID NO:2, see above) within the first peak of hydrophilicity (Figure 29a, peak I). The second peak of hydrophilicity (Figure 29a, peak II) is expected to contain the cleavage site yielding the p52 heparanase species. This is not surprising, considering the fact that these regions, are positioned at the surface of the heparanase molecule and are thus susceptible to proteolysis.

Figure 29c demonstrates the steps undertaken in constructing four basic nucleic acid constructs harboring a unique protease recognition and cleavage sequence of factor Xa - Ile-Glu-Gly-Arg↓ - or of enterokinase - Asp-Asp-Asp-Asp-Lys↓ downstream amino acids 119 or 157. *Aat*II-*Afl*II restriction fragments derived from these four basic constructs can be used to replace a corresponding region in any of the hpa constructs described herein (Figures 5a-e) and for that effect, any other construct harboring a *hpa* derived sequence. Figure 29b shows the modified heparanase species (pre-p56' and pre-p52') that contain these unique protease recognition and cleavage sequences (shaded regions) which enable proteolytic processing by the respective proteases to obtain homogeneously processed and highly active heparanase species (p56' and p52', respectively).

The above described constructs are highly suitable for expression of heparanase in any expression system which is characterized by secretion of the recombinant heparanase to the growth medium. Such a precursor enzyme can be readily and precisely processed into a mature active form of heparanase - p56' or p52'.

Although the invention has been described in conjunction with specific embodiments thereof, it is evident that many alternatives, modifications and variations will be apparent to those skilled in the art. Accordingly, it is intended to embrace all such alternatives, modifications and variations that fall within the spirit and broad scope of the appended claims.

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WHAT IS CLAIMED IS:

1. A genetically modified cell comprising a polynucleotide sequence encoding a polypeptide having heparanase catalytic activity, said cell expressing recombinant heparanase.

2. The genetically modified cell of claim 1, wherein said polynucleotide sequence is as set forth in SEQ ID NO:1 or a functional part thereof, said part encodes said polypeptide having said heparanase catalytic activity.

3. The genetically modified cell of claim 1, wherein said polypeptide includes an amino acid sequence as set forth in SEQ ID NO:2 or a functional part thereof having said heparanase catalytic activity.

4. The genetically modified cell of claim 1, wherein said polynucleotide sequence is selected from the group consisting of double stranded DNA, single stranded DNA and RNA.

5. The genetically modified cell of claim 1, wherein said cell is a bacterial cell.

6. The genetically modified cell of claim 5, wherein said cell is E. *coli*.

7. The genetically modified cell of claim 1, wherein said cell is an animal cell.

8. The genetically modified cell of claim 7, wherein said cell is an insect cell.

9. The genetically modified cell of claim 7, wherein said cell is a mammalian cell.

10. The genetically modified cell of claim 9, wherein said mammalian cell is selected from the group consisting of CHO cells, BHK21 cells, Namalwa cells, Dauidi cells, Raji cells, Human 293 cells, Hela cells,

Ehrlich's ascites cells, Sk-Hep1 cells, $MDCK_1$ cells, $MDBK_1$ cells, Vero cells, Cos cells, CV-1 cells, NIH3T3 cells, L929 cells and BLG cells.

11. The genetically modified cell of claim 8, wherein said insect cell is selected from the group consisting of High five and Sf21 cells.

12. The genetically modified cell of claim 1, wherein said cell is a yeast cell.

13. The genetically modified cell of claim 12, wherein said yeast cell is a methylotrophic yeast.

14. The genetically modified cell of claim 12, wherein said yeast cell is selected from the group consisting of *Pichia pastoris*, *Hansenula polymorpha* and *Saccharomyces cerevisiae*.

15. The genetically modified cell of claim 1, wherein said heparanase is human recombinant heparanase.

16. The genetically modified cell of claim 1, wherein said polynucleotide sequence is integrated in the cell's genome rendering the cell a stably transduced.

17. The genetically modified cell of claim 1, wherein said polynucleotide sequence is external to the cell's genome, rendering the cell transiently transduced.

18. The genetically modified cell of claim 1, wherein said polynucleotide sequence encodes in addition a signal peptide for protein secretion.

19. The genetically modified cell of claim 1, wherein said polypeptide includes a signal peptide for protein secretion.

20. A method of obtaining recombinant heparanase comprising the steps of genetically modifying a cell with an expression vector including a polynucleotide sequence encoding a polypeptide having heparanase catalytic activity, said cell expressing recombinant heparanase.

21. The method of claim 20, wherein said polynucleotide sequence is as set forth in SEQ ID NO:1 or a functional part thereof, said part encodes said polypeptide having said heparanase catalytic activity.

22. The method of claim 20, wherein said polypeptide includes an amino acid sequence as set forth in SEQ ID NO:2 or a functional part thereof having said heparanase catalytic activity.

23. The method of claim 20, wherein said cell is a bacterial cell.

24. The method of claim 23, wherein said cell is E. *coli*.

25. The method of claim 20, wherein said cell is an animal cell.

26. The genetically modified cell of claim 25, wherein said cell is an insect cell.

27. The genetically modified cell of claim 25, wherein said cell is a mammalian cell.

28. The method of claim 27, wherein said mammalian cell is selected from the group consisting of CHO cells, BHK21 cells, Namalwa cells, Dauidi cells, Raji cells, Human 293 cells, Hela cells, Ehrlich's ascites cells, Sk-Hep1 cells, $MDCK_1$ cells, $MDBK_1$ cells, Vero cells, Cos cells, CV-1 cells, NIH3T3 cells, L929 cells and BLG cells.

29. The method of claim 26, wherein said insect cell is selected from the group consisting of High five and Sf21 cells.

30. The method of claim 20, wherein said cell is a yeast cell.

31. The method of claim 30, wherein said yeast cell is a methylotrophic yeast.

32. The method of claim 30, wherein said yeast cell is selected from the group consisting of *Pichia pastoris*, *Hansenula polymorpha* and *Saccharomyces cerevisiae*.

33. The method of claim 20, wherein said heparanase is human recombinant heparanase.

34. The method of claim 20, wherein said polynucleotide sequence is integrated in the cell's genome rendering the cell a stably transduced.

35. The method of claim 20, wherein said polynucleotide sequence is external to the cell's genome, rendering the cell transiently transduced.

36. The method of claim 20, wherein said polynucleotide sequence encodes a signal peptide for protein secretion.

37. The method of claim 20, wherein said polypeptide includes a signal peptide for protein secretion.

38. The method of claim 37, further comprising the step of subjecting said cell to a substance which induces secretion into the growth medium of secretable proteins, thereby inducing secretion of said recombinant heparanase into the growth medium.

39. The method of claim 38, wherein said substance is selected from the group consisting of thrombin, calcium ionophores, immune complexes, antigens and mitogens.

40. The method of claim 39, wherein said calcium ionophore is calcimycin.

41. The method of claim 38, wherein said substance is phorbol 12-myristate 13-acetate.

42. The method of claim 20, further comprising the step of purifying said recombinant heparanase.

43. The method of claim 42, wherein said purification is effected in part by an ion-exchange column.

44. The method of claim 43, wherein said ion-exchange colun a Source-S column.

45. The method of claim 42, wherein said purification is 1 said cell.

46. The method of claim 42, wherein said purification is frc growth medium in which said cell is grown.

47. The method of claim 20, wherein said cell is grown in a l biotechnological scale of at least half a liter growth medium.

48. A method of purifying a recombinant heparanase 1 overexpressing cells or growth medium comprising the steps of adsor said recombinant heparanase on an ion-exchange column under low conditions, washing said column with low salt solution thereby eluting c proteins, and eluting the recombinant heparanase from said column by a gradient or higher salt concentration.

49. The method of claim 48, wherein said ion-exchange colun a Source-S column.

50. A method of activating a heparanase enzyme comprising step of digesting the heparanase enzyme by a protease.

51. The method of claim 1, wherein said protease is selected 1 the group consisting of a cysteine protease, an aspartyl protease, a se protease and a meatlloproteinase.

52. The method of claim 1, wherein said step of digesting

44. The method of claim 43, wherein said ion-exchange colun a Source-S column.

45. The method of claim 42, wherein said purification is i said cell.

46. The method of claim 42, wherein said purification is frc growth medium in which said cell is grown.

47. The method of claim 20, wherein said cell is grown in a l biotechnological scale of at least half a liter growth medium.

48. A method of purifying a recombinant heparanase i overexpressing cells or growth medium comprising the steps of adsor said recombinant heparanase on an ion-exchange column under low conditions, washing said column with low salt solution thereby eluting c proteins, and eluting the recombinant heparanase from said column by a gradient or higher salt concentration.

49. The method of claim 48, wherein said ion-exchange colun a Source-S column.

50. A method of activating a heparanase enzyme comprising step of digesting the heparanase enzyme by a protease.

51. The method of claim 1, wherein said protease is selected i the group consisting of a cysteine protease, an aspartyl protease, a se protease and a meatlloproteinase.

52. The method of claim 1, wherein said step of digesting

54. A method of *in vivo* inhibition of proteolytic processin heparanase comprising the step of *in vivo* administering a protease inhib

55. The method of claim 54, wherein said protease inhibitc selected from the group consisting of a cysteine protease inhibitor aspartyl protease inhibitor, a serine protease inhibitor and meatlloproteinase inhibitor.

56. A nucleic acid construct comprising a first nucleic segment encoding for an upstream portion of heparanase, a second frame, nucleic acid sequence encoding a recognition and cleavage sequ of a protease and a third, in frame, nucleic acid sequence encoding f downstream portion of heparanase, wherein said second nucleic sequence is in between said first nucleic acid sequence and said t nucleic acid sequence.